COMPOSITIONS AND METHODS FOR TREATING OR PREVENTING HIV INFECTION

This application claims the benefit of U.S. Provisional Application Nos. 60/491,258 filed July 31, 2003, 60/493,767 filed August 11, 2003, 60/496,908 filed August 22, 2003, and 60/501,832 filed September 11, 2003, which are hereby incorporated by reference in their entirety.

BACKGROUND OF THE INVENTION

Acquired Immune Deficiency Syndrome ("AIDS") is one of the most serious health threats confronting the human population today. AIDS is caused by a virus known as human immunodeficiency virus ("HIV") which presently includes HIV-1 and HIV-2. Over 40 million people are estimated to be living with HIV/AIDS. Current projections suggest that an additional 45 million people will become infected between 2002 and 2010. So far, it is believed that more 25 million people have died from AIDS.

Since its emergence in the 1970s, HIV has produced a continually growing global pandemic, and it has, thus far, defied all attempts to produce an effective vaccine. Although a number of drugs have been developed to treat the disease, all have limited usefulness, serious side effects, a high potential for resistance, and none have been identified so far which can cure or prevent it. HIV vaccine research has expanded over recent years, but success so far using HIV-based components has been limited. See, e.g., Graham et al., *J. Inf. Disease.*, 166:244-252, 1992; Belshe et al., *J. Inf. Disease.*, 183:1343-52, 2001; Horton et al., *J. Virol.*, 76:7187-7202, 2002; Gilbert et al., *Vaccine*, 21:2933-2947, 2003.

DESCRIPTION OF DRAWINGS

FIG. 1 (A-C). Comparison of cells from vaccinated versus non-vaccinated subjects, infected with the macrophage (CCR5) tropic HIV. A. A comparison of the mean + standard error measurement of the vaccinated versus non-vaccinated groups in cultures without autologous serum. (*, $p<0.05$) B. A comparison of the mean +

standard error measurement of the vaccinated versus non-vaccinated groups in cultures with autologous serum (*, $p< 0.05$; **, $p<0.01$). C. Comparison of the mean + standard error measurement of cells from vaccinated versus non-vaccinated subjects, infected with the T-cell (CXCR4) tropic HIV.

DESCRIPTION OF THE INVENTION

The present invention provides methods and compositions for treating and/or preventing HIV infection in a subject in need thereof. It features the use of poxviruses for therapy, prophylaxis, and diagnosis of HIV, as well as for any other medical or veterinary use associated with HIV and homologous viruses. The invention also provides for the use of poxviruses in the discovery of new agents to prevent and/or treat HIV infection.

A poxvirus or a component thereof, can be used to treat and/or prevent infection caused by any virus, preferably a lentivirus, such as HIV, that uses a CCR5 chemokine receptor for its infection of cells. This includes, but is not limited to, e.g., HIV-1 (e.g., clades A, B, C, D, and G, R5 and R5X4 viruses, etc.), HIV-2 (e.g., R5 and R5X4 viruses, etc.), simian immunodeficiency virus (SIV), simian/human immunodeficiency virus (SHIV), feline immunodeficiency virus (FIV), bovine immunodeficiency virus (BIV) (Wright et al., *Vet. Res. Commun.*, 26:239-50, 2002), HTLV-1, HTLV-2, etc. It can be used as a vaccine, adjuvant, therapeutic agent, in combination with other agents, or in any suitable manner to treat and/or prevent such infections.

Any poxvirus can be used in accordance with the present invention, including, but not limited to, orthopoxvirus, parapoxvirus, avipoxvirus, capripoxvirus, leporipoxvirus, suipoxvirus, etc. Orthopoxvirus, include, e.g., buffalopox, camelpox, cowpox, monkeypox, rabbitpox, raccoon pox, tatera pox, canarypox, fowlpox, vaccinia, variola, and vole pox. Vaccinia virus is the prototype of the genus Orthopoxvirus for the desired effects, but other poxviruses can be used in its place. Thus, although the disclosure below may be written in terms of vaccinia, any poxvirus can be utilized in accordance with the present invention.

Vaccinia is a double-stranded DNA (deoxyribonucleic acid) virus. All strains, derivatives, variants, mutations, naturally-occurring strains, genetically-engineered, recombinant, etc., of vaccinia can be used in accordance with the present invention. For more information on vaccinia and other poxvirus, see e.g., *Virology*, Fields et al., Volume 2, Chapters 74-75, Raven Press, 1990.

An amount of the poxvirus, such as vaccinia virus, can be administered to a subject in a quantity which is effective to achieve a therapeutic or prophylactic effect. The term "poxvirus," "vaccinia virus," etc., indicates that the virus (genome and protein coat) is administered to a subject. It can be administered in any effective form, including, e.g., as a live virus, as a live-attenuated virus, as a replication-deficient virus, as a viral extract not having any live viral particles, etc. Compositions comprising a poxvirus can be produced and utilized in any suitable manner, including, e.g., recombinant, naked DNA technology, etc.

The term "treating" is used conventionally, e.g., the management or care of a subject for the purpose of combating, alleviating, reducing, relieving, improving, eliminating, etc., one or more signs or symptoms associated with HIV infection. Treatment includes delaying the progression of HIV and its associated symptoms, thereby extending the life expectancy of an infected subject, and/or delaying or reducing the onset of symptoms associated with HIV infection. Treating can involve inhibiting, reducing, diminishing, etc., the replication and other events in the life cycle of the HIV virus.

The term "preventing" HIV infection indicates that a subject's susceptibility to HIV infection upon exposure to the virus is reduced or diminished as a result of the administration of the poxvirus. The subject's resistance to HIV infection is increased or improved by the poxvirus treatment since s/he is less likely to become infected by the virus. Any amount of improved resistance is useful, e.g., greater than 5-fold, greater than 7-fold, greater than ten-fold, etc., and any such improvement can be regarded as prevention.

A poxvirus, or component thereof, used in the present invention can be prepared routinely, or obtained from commercial sources. Attenuated strains are preferred. Attenuated strains are less able to cause disease, and are considered less virulent and weakened as compared to strains that are not attenuated.

Any strain of vaccinia virus, or components thereof, can be utilized to achieve a prophylactic and/or therapeutic effect, including, but not limited to, e.g., strains available from the ATCC, ECACC, or other virus collections, replication-competent, replication-deficient, non-replicating, attenuated strains, modified vaccinia Ankara (MVA), vaccinia virus Ankara, NYVAC (ATCC No. VR-2559) replication-deficient vaccinia viruses, VV Copenhagen, VV Western Reserve, VV Wyeth (ATCC No. VR325), Elstree, strains deficient in vCCI (Reading et al., *J. Immunol.*, 170:1435-42, 2003), and/or vGF, strains comprising one or more copies of the 17K myristyloprotein, poxvirus strains, CCR5-dependent poxvirus strains, etc. Dryvax®, a vaccinia (smallpox) vaccine currently licensed in the United States, is a lyophilized, live-virus preparation of infectious vaccinia virus (Wyeth Laboratories, Inc., Marietta, Pennsylvania). Other strains which have been used include, but are not limited to, e.g., Lister, Bordeaux, Paris, Massachusetts 999, New York, Temple of Heaven, Patwadangar, Ikeda, Bern, Vienna, Bohemia, Finland, Hamburg, Budapest, Aosta, Spain, Sweden, B-51, Tashkent, EM-63, LE-IVP (Lister), etc. See, also, *Smallpox and its Eradication*, Fenner et al., WHO, Geneva, 1988, e.g., Chapter 11. Other strains include, e.g., MVA-BN (modified vaccinia Ankara – Bavarian Nordic) (ECACC V00083008; WO 02/42480), MVA-Vero (US 20030013190), MVA-NH, MVA 572 (ECACC V94012707), LC16m8, and ACAM1000 (ATCC Deposit No. PTA-3321; WO 02/085411). Any strain of canarypox can be utilized as well, including attenuated canarypox virus such as, e.g., ALVAC (ATCC No. VR-2547).

Deposited strains also include, e.g., ATCC Nos. VR-117 (CL), VR-118 (Lederle-Chorioallantoic), VR-119 (WR (Mouse Neurotropic), VR-1354 (WR (NIH TC-adapted), VR-1431 (P-4), VR-1441 (IHD-W), VR-1508 (Modified vaccinia virus Ankara (MVA)), VR-1536 (New York City Department of Health Laboratories (Wyeth-calf adapted)), VR-1549 (Elstree (Lister Vaccine)), VR-156 (IHD), VR-2010 (AS), VR-2031 (Vtk-79), VR-2034 (S-variant), VR-2042 (vP-7), VR-2043 (vP-9), VR-2292 (SLZ103[recombinant Vaccinia virus (WR)]), VR-2379 (Rpmuhr+ [recombinant of Utrecht strain Rpuhr23]), VR-2589 (VVtm1:hPC1 [recombinant Vaccinia virus, in vitro construct]), VR-302 (Brighton), VR-3103 (IHD-W Dts 16 [Vaccinia ts-mutant]), VR-3109 (IHD-W Dts 46 [Vaccinia ts-mutant]), VR-3110 (IHD-W Dts 2 [Vaccinia ts-mutant]), VR-3113 (IHD-W Dts 17 [Vaccinia ts-mutant]),

VR-3121 (IHD-W Dts8 [Vaccinia ts-mutant]), VR-3126 (IHD-W Dts 33 [Vaccinia ts-mutant]), VR-3129 (IHD-W Dts 48 [Vaccinia ts-mutant]), VR-3130 (IHD-W Dts 4 [Vaccinia ts-mutant]), VR-3139 (IHD-W Dts 50 [Vaccinia ts-mutant]), VR-3142 (IHD-W Dts 10 [Vaccinia ts-mutant]), VR-3144 (IHD-W Dts20), VR-3147 (IHD-W Dts 35 [Vaccinia ts-mutant]), VR-3148 (IHD-W Dts 40), VR-3154 (IHD-W Dts71 [Vaccinia ts-mutant]), VR-3160 (IHD-W Dts52 [Vaccinia ts-mutant]), VR-3161 (IHD-W Dts 57), VR-3165 (IHD-W Dts 77), VR-3166 (IHD-W Dts 82), VR-3169 (IHD-W Dts97 [Vaccinia ts-mutant]), VR-3175 (IHD-W Dts 78 [Vaccinia ts-mutant]), VR-3176 (IHD-W Dts 83 [Vaccinia ts-mutant]), VR-3178 (IHD-W Dts 93 [Vaccinia ts-mutant]), VR-3196 (IHD-W Dts 95 [Vaccinia ts-mutant]), VR-587 (Yaba monkey tumor virus deposited as Yaba monkey tumor virus, Yatapoxvirus (Roswell Park-Yohn)), VR-838 (Raccoonpox virus, Orthopoxvirus (Herman)).

A vaccinia virus is a preferred poxvirus in accordance with the present invention, but other poxviruses can also be used to treat and/or prevent HIV. For example, any poxvirus which expresses a gp120-like or TAT-like polypeptide, or which depends on CCR5 for entry into a cell can be used in accordance with the present invention.

Vaccinia virus can be administered to subjects according to any regimen which is effective for treating and/or preventing HIV infection. The particular dosages (i.e., effective amounts), and number and frequency of vaccinations can be determined routinely.

An effective amount of virus, or virus component, is the quantity of virus, or virus component, which is useful to achieve the desired purpose, e.g., to treat and/or prevent HIV infection. These amounts can be determined routinely. Effective amounts can be the same or less than the amounts currently used to achieve pox immunity with a pox vaccine. For example, Dryvax™ is commonly used at a potency of 100 million pock-forming units (pfu)/ml for primary vaccination for smallpox. Any effective amount can be used in accordance with the present invention, e.g., about 10^5-10^9 pfu/ml. The quantities of the particular virus which is utilized can be adjusted and determined routinely, e.g., to eliminate or reduce adverse reactions associated with the virus, as well as depending on the health of the patient receiving the treatment.

The specific dose level and frequency of dosage may vary, and can depend upon a variety of factors, including the activity and state of the specific poxvirus, e.g., whether it is live, heat-inactivated, attenuated, etc., its metabolic stability and length of action, rate of excretion, mode and time of administration, and the age, body weight, general health, gender, diet, and particular condition of the subject undergoing treatment or prevention.

Poxvirus can be administered in any form by any effective route, including, e.g., oral, parenteral, enteral, intraperitoneal, topical, transdermal (e.g., using any standard patch), ophthalmic, nasally, local, non-oral, such as aerosal, spray, inhalation, percutaneous (epidermal), subcutaneous, intravenous, intramuscular, buccal, sublingual, rectal, vaginal, intra-arterial, mucosal, and intrathecal, etc. It can be administered alone, or in combination with any ingredient(s), active or inactive.

Any subject can be administered a poxvirus in accordance with the present invention, including subjects who have been exposed to HIV, but have not yet developed HIV infection, as well as subjects who have progressed to one or more of the clinical symptoms of HIV infection (e.g., AIDS). In addition to treating and/or preventing HIV infection in humans, a poxvirus can be used to treat other organisms (e.g., non-human primates, cats, etc.) infected with HIV, or HIV-related viruses, such as SIV, SHIV, or FIV. Thus, subjects who can be treated include, e.g., mammals, humans, monkeys, apes, chimpanzees, gorillas, cats, dogs, mice, rats, etc.

Subjects, who have been exposed to HIV virus, or who are at risk for developing the disease, are particular candidates for poxvirus vaccination. For instance, a subject who has not yet tested positive, but has been exposed to HIV, can be administered vaccinia virus as a prophylactic/therapeutic approach. Individuals at high-risk for the disease, such as sexually-active individuals, subjects in parts of the world where HIV infection is high, subjects receiving blood and/or other invasive medical procedures, can also receive vaccination to increase their resistance to HIV infection.

In addition to administering the whole poxvirus, components of it can also be administered in accordance with the present invention. By the phrase "component," it is meant any part of the virus, which is less than the whole virus genome, including

particular nucleic segments of its genome, as well as any product which is produced using the viral genome. This includes modifications to polypeptides encoded for by the virus.

Components include polypeptides comprising the virus, such as envelope proteins, processing enzymes, structural proteins, nucleic acid synthesis enzymes, glycoproteins, carbohydrates, lipids, antigens or antigenic fragments of the virus, etc. Also included are nucleic acid fragments of the whole genome, including fragments comprising complete gene sequences, control sequences, etc.

Components includes one or more of the over about 198 open reading frames (ORF) and about 268 genes that have been identified in vaccinia and other poxvirus. Components include one or more of the genes and products thereof described in, but not limited to, Antoine et al., *Virology*, 244:365-396, 1998, and Goebel et al., *Virology*, 179(1):247-266, 1990 for vaccinia virus; Willer et al., *Virology*, 264(2):319-43, 1999 for Leporipoxvirus Shope fibroma virus (SFV); Cameron et al., *Virology*, 264(2):298-318, 1999 for myxoma virus; Shchelkunov et al., *Virology*, 297(2):172-94, 2002 for monkeypox virus; Shchelkunov and Totmenin, *Virus Genes*, 9(3):231-45, 1995 for variola, Massung et al., *Virology*, 201(2):215-40, 1994. For example, the polypeptide coding for the 17K myristylprotein, and which has amino acid sequence homology to gp120, can be used alone or in combination with other antigens, etc., in accordance with the present invention. See, e.g., Antoine et al., 1998; Barrett et al., *Seminars in Immunol.*, 13:73-84, 2001. See, also Tables 1 (from Goebel et al., *Virol.*, 179:247-266, 1990) and 2 (from Antoine et al., *Virol.*, 244:365-396, 1998). Moreover, one or more of the aforementioned genes and open reading frames can be deleted from a vaccinia virus, e.g., to eliminate a toxic or other undesirable effect of an administered virus.

A useful composition can comprise one of the components of a poxvirus, including one or more of the components described in Tables 1 and 2. These can be individual purified and then combined into a therapeutic or prophylactic composition, or extracts can be prepared from viral particles and treated as desired. The individual components can be purified from the viral particles, or produced recombinantly, e.g., where a target gene is cloned, expressed in a host cell under conditions where the polypeptide is manufactured by the cell, and separating and purifying the polypeptide

accordingly to conventional methods. Components can also be administered as naked DNA. See, e.g., U.S. No. 6,413,942.

The therapeutic and/or prophylactic effect achieved with the poxvirus can be independent of an immunological response to it. For example, the purpose of ordinary smallpox vaccination is to elicit an immune response by the host. This response is both humoral and cellular, involving the generation of specific antibodies and immune cells (such as T-cells, cytolytic or cytotoxic T lymphocytes, etc.) which protect a host from future invasion by the smallpox virus. While the present invention is not bound by any mechanism through which the poxvirus achieves its therapeutic and/or prophylactic effect, it can be mediated through a pathway separate from the immune response and not require cellular or humoral immunity. For example, poxvirus, or a component thereof, can directly block or inhibit the ability of a HIV to infect a cell. In this respect, the poxvirus, or component of it, acts as an antagonist, blocker, etc., of HIV's ability to infect target cells. HIV usually activates a G-protein-coupled signal pathway cascade. Poxvirus can interfere with this pathway or modify it such a way that the cell is more difficult to infect, thereby increasing its resistance to the HIV virus. Consequently, the effective amounts of a poxvirus, or component thereof, can differ from the amounts that are ordinarily used when the objective is to achieve a humoral and/or cellular immune response.

Vaccination with vaccinia can be associated with adverse reactions. Those at highest risk include, e.g., pregnant women, immunocompromised patients (e.g. HIV-positive), and persons who have atopic dermatitis or eczema. Strains which are attenuated or otherwise modified to reduce adverse effects are especially useful in accordance with the present invention, e.g., for administration to persons at risk for adverse effects.

Modified strains of vaccinia can be utilized that are deficient, mutated, engineered, etc., in one or more of the about 198 open reading frames (ORF) and/or about 268 genes that comprise vaccinia (depending on the strain or variant). In addition, genes can be inserted into vaccinia, including, one or more copies of a vaccinia gene of interest (e.g., 17K myristylprotein, vCCI), and/or genes coding for all or part of an HIV proteins, such as gp120 or gp40.

The present invention also provides methods of treating and/or preventing HIV infection in a subject in need thereof, comprising, e.g., administering multiple doses of a poxvirus, or components thereof, to a subject, wherein each dose is administered at a time interval from the previous dose, and are effective to maintain a therapeutic effect, or to maintain protection against HIV infection. As discussed above, a dose of the poxvirus, or component thereof, is the amount of virus which is useful for accomplishing the therapeutic or prophylactic effect. More than one dose can be administered to the subject in order to maintain the therapeutic efficacy of the treatment, or to maintain protection against HIV infection. For example, smallpox immunization is usually achieved by a single vaccination with a booster every 5-10 years. To maintain protection against HIV, more frequent vaccination can be used, e.g., multiple times a year; at least twice a year, yearly, every two years, every three years, more than once every less than five years, more than once every less than ten years, etc. The periods between the separate and sequential vaccinations can be referred to as "time intervals." These intervals can be spaced apart by any desired time period which is effective to maintain protection or therapeutic efficacy in treating an infected subject. The intervals can be predetermined or preset, where they are already specified, or they can be determined by monitoring the progress of a subject, e.g., using blood serum to measure poxvirus antibody titer, or HIV titer in an infected subject. The frequency of vaccination utilized to achieve efficacy may vary depending upon multiple factors, including, e.g., person-to-person variations in the immune system, the stage of HIV infection, the potency of the virus or vaccine, etc, and may be as often as every 3 months to once every 5 years.

The present invention also provides methods of treating and/or preventing lentivirus infection in a subject in need thereof, comprising: administering an effective amount of a poxvirus or component thereof, wherein said amount is effective to treat and/or prevent lentiviral infection, with the proviso that a lentivirus nucleic acid, such as HIV, is not contained in the poxvirus genome. This excludes, e.g., a poxvirus which is utilized as a vector to administer HIV nucleic acid, such as when HIV nucleic acid is inserted into the poxvirus genome.

The present invention also provides methods of identifying a component of a poxvirus, or a poxvirus-associated agent, which interferes with HIV infection, and

components and agents identified thereby. Interfering with HIV infection indicates that the agent or component decreases, reduces, diminishes, lessens, etc., the ability of a susceptible cell or organism to become infected with HIV virus as compared to the same cell or organism in the same conditions, but in the absence of the agent or component. Interference with HIV infection can occur at any level, e.g., by blocking the ability of HIV to attach to its receptor(s) on a cell, by blocking the ability of HIV to be taken into a cell, by blocking viral function once inside the cell, by blocking viral infection, etc. The invention is not limited by the mechanism through which HIV interference is achieved. By interfering with HIV infection, the cell's or organism's resistance to HIV is increased.

These methods can involve one of more of the following steps in any effective order, e.g., (1) contacting a cell or organism which is susceptible to HIV infection with poxvirus, or a component thereof, or a poxvirus-associated agent, (2) contacting said cell or organism with HIV under conditions effective for said HIV to infect said cell or organism, and, (3) (a) determining whether said cell or organism is resistant to HIV infection, whereby said agent is identified as interfering with HIV infection, or (3) (b) identifying the poxvirus, or component thereof, which confers resistance to HIV infection. The term "organism" as used herein indicates a fully-gestated animal.

The method can also involve a step of identifying the poxvirus, or a component thereof, as the agent which confers resistance to HIV infection. Identifying the poxvirus, or component thereof, which confers resistance to HIV infection, indicates that the poxvirus is positively determined or ascertained to provide protection or resistance against HIV. This indicates a positive result in the method.

Agents can be tested for their ability to interfere with HIV infection in any suitable system, including whole animals and cell culture. Animal cells useful in the present invention are those which are susceptible to HIV infection, i.e., they are capable of being infected by the HIV virus. They can be naturally-susceptible, or genetically-engineered to confer susceptibility, e.g., by expressing HIV receptor (CCR5, CD4, etc.), or by grafting on the human immune system. Any methods for testing whether a cell or organism is infected with HIV can be used, e.g., measuring

anti-HIV antibody titer (e.g., gp120 antibodies), reverse transcriptase protein or nucleic acid, or any other polypeptide or nucleic acid.

Any suitable animal model for testing the efficacy and dosage of a poxvirus (or component thereof) can be used in accordance with the present invention. These include, but are not limited to, e.g., SCID mice reconstituted with human immune system components (e.g., peripheral blood lymphocytes) [e.g., Zhang et al., *Proc. Natl. Acad. Sci.*, 93:14720-14725, 1996, using SCIC.bg mice], chimpanzees infected with HIV-1, macaque monkeys infected with SIV, HIV2, or chimeric SIV/HIV [e.g., Johnson, *Curr. Opin. Immunol.*, 8(4):554-560, 1996], cats infected with feline immunodeficiency virus, HIV-1 transgenic mouse model [e.g., mice which have integrated molecular clone pNL4-3 containing 7.4 kb of the HIV-1 proviral genome deleted in the gag and pol genes (Dickie et al., *Virology*, 185:109-119, 1991; transgenic mice carrying an HIV provirus, optionally with deletion of one or more HIV genes (Tinkle et al., *J. Clin. Invest.*, 100(1):32-9, 1997)], HIV-1 transgenic rat model, human CD4 transgenic rat model, horse infected with EIAV, sheep infected with visna virus, goats infected with CAEV, etc. See, also, *The Retroviridae*, J. A. Levy, ed., Plenum Press, 1993, e.g., Chapters 3, 4, and 5.

A vaccinia virus-associated agent is any substance which is produced in response to a vaccinia infection, or in response to inhalation, injection, ingestion, etc., of any vaccinia virus, or component thereof. This substance can be present in a culture medium in which cells exposed to vaccinia have been cultured, or can be present in blood serum when harvested from an organism exposed to vaccinia. The present invention provides compositions which comprise such substances.

The invention also provides combinations of pharmaceutical agents for treating and/or preventing HIV, e.g., poxvirus, or a component thereof, and an agent which is used to treat HIV, such as a protease inhibitor or a reverse transcriptase inhibitor. Examples of the latter classes of drug, include, but are not limited to, saquinavir, ritonavir, indinavir, nelfinavir, amprenavir, lopinavir, atazanavir, fosamprenavir, tipranavir, AZT, ddI, ddC, ddT, 3TC, nevirapine, delavirdine, etc. The active agents can be present in the same dosage unit (e.g., a composition), or can be used as separate dosage units.

In addition, a poxvirus, such as vaccinia, can be administered in combination with HIV nucleic acid. The HIV nucleic acid can be physically joined to the poxvirus genome , or it can be administered as a separate component. For example, HIV nucleic acid (e.g., coding for gp120 or another viral antigen) can be administered at the same time as a poxvirus, but as a physically separated entity, or it can be administered at subsequent times after receiving only poxvirus) as part of a regimen for treating and/or preventing HIV infection.

The present invention also provides methods of making a poxvirus composition for conferring resistance to HIV infection or treating HIV infection, , comprising, one or more of the following steps in any effective order, e.g., preparing a composition comprising poxvirus, or a poxvirus component thereof, and/or identifying that the poxvirus, or component thereof, confers resistance to, or treats, HIV infection. As mentioned earlier, the identifying step indicates obtaining a positive result in finding that the poxvirus (e.g., vaccinia), or component thereof, provides resistance, protection, treatment, etc., against the HIV virus.

The preparation of a poxvirus composition can be carried out routinely, e.g., according to conventional methods used for vaccine manufacture. Preparing includes culturing poxvirus, isolating poxvirus, putting poxvirus into a form suitable for administration (oral, injection, nasal, etc.), making poxvirus components recombinantly, etc. The prepared poxvirus (or components of it) can be assayed for its ability to confer resistance to HIV infection to an organism challenged with it or provide a therapeutic effect. By this, it is meant that a sample of the prepared composition is tested to determine its titer, concentration, potency, etc., in making a subject, to whom it is administered, "resistant" to the HIV virus, or for its therapeutic effect. The assay step can be carried out on every batch, or only selected batches, etc. A purpose of this step is, e.g., to confirm that the manufactured poxvirus possesses an anti-HIV activity for which it is to be administered. Any suitable assay or testing method can be utilized, e.g., in vitro methods of evaluating its efficacy or potency. For instance, the determining step can involve, e.g., challenging said organism, or cells derived from it, with infectious HIV, and detecting the expression in said organism or cells of gp120, HIV reverse transcriptase, p24, infectious HIV particles, and/or HIV nucleic acid. By "challenge" it is meant the cells or organism are placed

in contact wit the HIV virus under conditions which are effective to become infected by it. These conditions will vary, depending upon how the assay is specifically accomplished.

When poxvirus is administered to a host, it can elicit a cellular response that is responsible or associated with the host's subsequent ability to resist HIV infection and/or treat HIV infection. This response can be measured, and used as index or marker to assess the efficacy of the poxvirus, and/or to determine effective amounts of it for the desired purpose (i.e., treating or preventing HIV infection). The appearance of one or more of the following "markers" can be modulated (e.g., elicited, stimulated, down-regulated, up-regulated, etc) by poxvirus, and associated with its anti-HIV effect, thereby making the marker useful as an indicator of poxvirus efficacy. By the term "marker," it is meant any measurable response to a poxvirus, including its effect on HIV's ability to infect and replicate in a cell, as well as on the host's immune system and the cells which comprise it. These markers, include, but are not limited to; one or more of the following agents, activities, responses, pathways, etc.:

- CD4 expression, e.g., measuring the amount of CD4 present in a cell-type that is susceptible to HIV infection

- HIV coreceptor expression, e.g., CCR5 or CXCR4 chemokine receptor, including its cell-surface expression

- Cytokine receptors

- Virus-specific CTLs (cytolytic or cytotoxic T-cells, including CD8+ T-cells) which are capable of lysing HIV infected cells (cells can be co-infected with poxvirus and HIV, or infected by HIV alone)

- CD8 cells

- Cytokines, including mediators and regulators of innate immunity, such as interferons, type I interferon, interleukins, interleukin-15, interleukin-12, tumor necrosis factor, interleukin-1, interleukin-6, interleukin-10, etc.; and mediators and regulators of specific immunity, such as interleukins, interleukin-2, interleukin-4, transforming growth factor-beta, interferon-gamma, lymphotoxin, interleukin-5, etc.

- Chemokines (a large family of structurally homologous cytokines, that, e.g., stimulate leukocyte motility and directed movement), including, but not limited to,

the C-C and C-X-C families. Examples of chemokines, include, but are not limited to, e.g., interleukin 8, Gro, platelet basic protein, epithelial-derived neutrophil attractant 78, platelet factor 4, interferon-gamma-induced protein 10, stromal cell-derived factor-1, monocyte chemotactic proteins 1, 2, and/or 3, RANTES, monocyte inflammatory protein 1-alpha and 1-beta ("MIP"), eotaxin, lymphotaxin, etc.

- Th1/Th2 phenotype and cytokine secretion pattern. Effector T-cells (e.g., CD4+ helper T-cells) can be categorized, on the basis of the cytokines they secrete, into Th1 and Th2 cells. Th1 cells secrete, e.g., interferon-gamma, lymphotoxin-alpha, TNF-beta, IL-2, IL-10, and CCR5 ligands, such as RANTES and MIPS. Th2 cells secrete, e.g., IL-4, IL-5, IL-6, IL-9, IL-10, IL-13, etc. Th1 and Th2 cells also include resting, but polarized T-cells (i.e., committed to a Th type). In addition to cytokine production profiles, there are a number of cell surface markers that can be used to differentiate between Th1 and Th2 subtypes. For example, Th1 cells express both components of IL-12 receptor chains (beta1 and beta2), while Th2 cells exhibit IL-12R-beta1. Th2 cells exhibit both IFN-gamma receptor chains (a and b), while Th1 cells express IFN-gamma-R-alpha. Th2 cells appear to express a fully functional IL-1 receptor, and ST2L/T1, an IL-1R-like molecule, is found on Th2 cells. Chemokine receptors CXCR-3 and CCR-5 are also characteristic of Th1 cells, while CXCR-4, CCR-3, CCR-4, CCR-7 and CCR-8 are associated with Th2 cells. CD30, a member of the TNF superfamily, is associated with Th2 cells. The Th1/Th2 pattern can be polarized by poxvirus administration, resulting in a phenotype that favors the secretion, etc., of cytokines that inhibit HIV infection and/or render cells resistant to infection. One or more of the aforementioned molecules can be utilized as markers of poxvirus efficacy

- Antibodies that specifically recognize HIV, e.g., neutralizing antibodies

- Antibodies that specifically recognize poxvirus

- Complement control protein. Vaccinia virus encodes a secreted complement control protein (VCP, 35-kDa) protein with sequence homology to the SCR-containing complement control protein superfamily. It binds C3b and C4b, and interferes with the complement cascade by providing cofactor activity for the cleavage of C3 and C4 by factor I, and by accelerating the decay of the C3 converse of both the alternative and, more effectively, the classical pathway of complement

activation. VCP may suppress the complement system or their receptor expression, rendering the host less susceptible to the complement-enhancement of HIV infection

- Activation state of a cytokine receptor, e.g., CCR5 receptor or other HIV chemokine coreceptor. For example, poxvirus can interfere with CCR5 activation after HIV binding, e.g., by modulating tyrosine kinase feedback pathways

- One or more of the vaccinia proteins listed in Tables 1 and 2. This includes any poxvirus-encoded protein that specifically interferes with CCR5/CD4/gp120 interactions, including, e.g., vaccinia encoded CC chemokine binding proteins and/or IFN-gamma receptor-like protein

- RNA interference with HIV expression/replication in infected cell

- Alpha-defensins 1, 2, and/or 3

- Soluble factors including those produced by CD8+ lymphocytes and sometimes referred to as CAF

- Interference with the HIV life cycle, including viral entry, import into the host cell nucleus, viral integration into host genome, Rev-dependent and Rev-independent transport from the host nucleus, replication, gene expression, RNA splicing, etc

- Inhibiting HIV replication, including its ability to make copies of itself in the cell, and for productive viral particles to be extruded into the blood

- Inhibiting the ability of HIV to infect a cell, e.g., to bind to CD4 and/or its coreceptor, for the envelope protein to fuse with the host cell membrane, etc.

- Modulating gene expression of the HIV virus, including modulating regulatory genes (e.g., tat and rev), accessory genes (e.g., vif, vpu, vpr, and nef), structural genes (e.g., gag, pol, and env), inner core polypeptides (e.g., gag, p17, p24, p7, and p9), viral enzymes (pol, reverse transcriptase, protease, and integrase), and envelope proteins (e.g., env, gp120, and gp41). The phrase "gene expression" is used broadly to mean any step in the pathway from viral RNA to protein synthesis, and therefore includes all regulatory processes, transcription, translation, polypeptide processing, etc.

- Modulating activity of a HIV encoded polypeptide, including, tat, rev, vif, vpu, vpr, nef, gag, p17, p24, p7, p9, pol, reverse transcriptase, protease, integrase, env, gp120, gp41, etc.

- Modulating viral regulatory sequences, such as RRE, cis-acting repressive sequences (CRS), and inhibitory/instability RNA sequences (INS)

- Any cell or tissue of the immune system, including, but not limited to, lymphocytes, B lymphocytes, T lymphocytes, helper T cells, cytotoxic (or cytolytic) T cells ("CTL), natural killer (NK) cells, naïve T cells, memory T cells, CD4+ helper T cells, CD8+ CTLs, monocytes, macrophages, antigen-presenting cells (APCs), dendritic cells, granulocytes, etc.

The present invention also provides kits comprising a poxvirus. For example, a kit for preventing HIV infection, comprising: an effective amount of a poxvirus, and instructions for administering an effective amount of said poxvirus to a subject to prevent HIV infection; and a kit for treating HIV infection, comprising: an effective amount of a poxvirus, and instructions for administering an effective amount of said poxvirus to a subject to treat HIV infection. The instructions can provide any information that is useful for directing the administration of the poxvirus for the desired purpose.

The present invention also provides methods of advertising, licensing, selling, purchasing, etc., a poxvirus for the purpose of treating and/or preventing HIV infection. Methods can comprise, one or more of the following steps in any effective order: e.g., displaying information (a) comprising instructions for administering a poxvirus for treating and/or preventing HIV infection or (b) comprising a description of the use of poxvirus for treating and/or preventing HIV infection, in a printed or computer-readable medium (e.g., on the Web, Internet, personal computer, server, etc); offering for sale a poxvirus for treating and/or preventing HIV infection in a printed or computer-readable medium; accepting an offer to purchase poxvirus for said use in a printed or computer-readable medium.

EXAMPLES

The following experiments were performed in the laboratory of Dr. Beda Brichacek and Dr. Michael Bukrinsky of the Department of Microbiology and Tropical Medicine, The George Washington University, Washington D.C. 20037.

Methods

Subject selection and specimen collection.

Twenty subjects were chosen for inclusion in the study. Ten subjects had been immunized with vaccinia within the previous 3 to 6 months, and ten subjects had never been immunized with vaccinia. All subjects were healthy and had a negative HIV test within the previous year. No subjects of northern European descent were used in order to avoid the potentially complicating factor of including a subject who might be homozygous for the CCR5-delta32 mutation. Two tubes of heparinized blood and 1 serum separator tube were collected. All blood samples from all subjects were drawn within 6 hours of each other, and were immediately processed to separate the PBMCs using standard methods of Ficoll-Hypaque centrifugation.

Cell culture preparation.

PBMCs were centrifuged at 1200 rpm for 11 minutes and resuspended in RPMI tissue culture medium + 10% fetal calf serum + 10 μg/ml gentamicin at a concentration of about 1-3 x 10^6 cells/ml with a final concentration of 2 x 10^6 cells/culture. Cell cultures were incubated in a CO_2 incubator. On the second day, one of the utilized strains of HIV was mixed with either culture medium or serum from each individual subject and incubated on ice for 7 hours after which 175 μl of each mixture was added to the autologous cell cultures. The next day 1 ml of cell culture media was added and the cultures were incubated for 5 hours to dilute the viral inoculum and to allow the virus to detach. The supernatant was carefully aspirated and 1 ml of fresh media was added before the cultures were spun down at 1000 rpm for 7 minutes. The supernatant was again aspirated and 2 ml of fresh media was added to each culture. 150 μl of supernatant for RT analysis was aspirated from each culture tube on days 2, 5, 8 and 10, and if needed, up to an additional 1 ml was aspirated and replaced with fresh media. On day 2, PHA was added to the tubes of

culture series F to act as a cell activator. On day 5, 2 ml of supernatant was removed from each of tubes of culture series F and replaced with 2 ml media + human serum + IL-2.

Reverse Transcriptase (RT) analysis.

The measurements of viral replication were performed by standard RT assays using tritiated thymidine as described in numerous articles in the scientific literature. See, e.g., Rey et al., *Virology*, 181(1), 165-71, 1991.

Results

All results are based on RT analysis using tritiated thymidine, and are given in counts per minute (CPM).

Culture Series A, the control, demonstrated no viral replication in any cultures.

Culture Series B (without serum; Fig. 1A) demonstrated a significant reduction of viral replication in most cultures from vaccinated subjects when compared to unvaccinated subjects. Two subjects (1 and 10) showed a complete lack of viral replication, comparable to the controls in culture series A. One subject was excluded from all analyses when it was subsequently discovered that the subject had had a highly anomalous reaction to the vaccinia immunization with recurrent skin lesions for months afterward. This suggested an inadequate immune response to the vaccinia, and this subject correspondingly did not show any protection against HIV in cell culture, demonstrating viral replication comparable to unvaccinated subjects.

Culture Series C (with serum; Fig. 1B) also demonstrated a significant reduction of viral replication in most cultures from vaccinated subjects, when compared to unvaccinated subjects. The same two subjects (1 and 10) noted in culture series B also had no demonstrable viral replication, comparable to the controls in culture series A. The addition of autologous serum in culture series C further enhanced the difference between vaccinated and unvaccinated subjects when compared to culture series B (no serum).

Culture Series D, E and F, using the T-cell (CXCR4) tropic HIV (Fig. 1C), demonstrated no difference between vaccinated and unvaccinated subjects, including

the two subjects (1 and 10) who were resistant to infection by the macrophage (CCR5) tropic HIV in culture series B and C. As stated in the methods section, care was taken in the selection of subjects to avoid those of northern European descent who might be homozygous for the CCR5-delta32 mutation, so this cannot be an explanation for the described resistance. There was also no difference noted between the addition of serum and no serum (cultures D and E).

Discussion

By at least day 10, there is a statistically significant difference between the vaccinated and non-vaccinated subjects in culture series B and C (p=.035 and .013 respectively) that increases by day 13 (p=.017 and .008 respectively), indicating a resistance to infection by HIV in the vaccinated subjects (Fig. 1). Subjects 1 and 10 demonstrated total resistance to macrophage (CCR5) tropic HIV infection in both culture series B and C, with RT measurements equal to the non-HIV infected control (culture series A). The fact that the same result was achieved in both sets of cultures, while infection was easily achieved with the T-cell (CXCR4) tropic HIV in cultures D, E and F, indicate these finding were not the result of laboratory error.

Without further elaboration, it is believed that one skilled in the art can, using the preceding description, utilize the present invention to its fullest extent. The following preferred specific embodiments are, therefore, to be construed as merely illustrative, and not limitative of the remainder of the disclosure in any way whatsoever. The entire disclosure of all applications, patents and publications, cited above and in the figures are hereby incorporated by reference in their entirety, including of U.S. Provisional Application Nos. 60/491,258 filed July 31, 2003, 60/493,767 filed August 11, 2003, 60/496,908 filed August 22, 2003, and 60/501,832 filed September 11, 2003.

TABLE 1

THE OPEN READING FRAMES OF VACCINIA VIRUS

Gene[a]	Translation Start	Translation Stop[b]	Size aa	Size M_r[c]	Characteristics[d]	References
C23L*	5008	4277	244	26.4	Nonessential; B29R Acidic[e] (4.2)	Perkus, *et al.* (1990b)
C22L*	6113	5748	122	13.6	Nonessential; B28R Hydrophobic N-terminus	Perkus, *et al.* (1990b)
C21L*	6815	6477	113	13.4	Nonessential; B27R	Perkus, *et al.* (1990b)
C20L*	7132	6824	103	12.5	Nonessential; B26R Basic (9.0)	Perkus, *et al.* (1990b)
C19L*	7856	7080	259	30.5	Nonessential; B25R Hydrophobic N-terminus	Perkus, *et al.* (1990b)
C18L*	8693	8244	150	17.5	Nonessential; B24R Acidic (4.8)	Perkus, *et al.* (1990b)
C17L*	9947	8790	386	44.9	Nonessential; B23R	Perkus, *et al.* (1990b)
C16L*	10539	9997	181	21.0	Nonessential; B22R	Perkus, *et al.* (1990b)
C15L*	11153	10881	91	10.5	Nonessential; B21R	Perkus, *et al.* (1990b)
C14L	12212	11967	82	9.3	Nonessential Basic (9.2)	Perkus, *et al.* (1990b)
C13L	12510	12316	65	7.4	Nonessential Acidic (4.0)	Perkus, *et al.* (1990b)
C12L	13733	12675	353	40.4	Serine Protease Inhibitor Nonessential Acidic (4.8)	Kotwal and Moss (1988b) Perkus, *et al.* (1990b)
C11R	14178	14603	142	15.8	Growth Factor Nonessential EGF-like type A domain Hydrophobic C-terminus	Blomquist, *et al.* (1984); Brown, *et al.* (1985); Reisner (1985) Buller, *et al.* (1988); Perkus, *et al.* (1990b)
C10L	15754	14762	331	38.5	Nonessential Acidic (4.5)	Perkus, *et al.* (1990b)
C9L	18136	16235	634	74.7	Nonessential	Perkus, *et al.* (1990b); Kotwal and Moss (1988b)
C8L	18733	18182	184	21.6	Nonessential Acidic (4.4)	Kotwal and Moss (1988b); Perkus, *et al.* (1990b)
C7L	19257	18808	150	18.0	Nonessential Host range function	Kotwal and Moss (1988b); Perkus, *et al.* (1990a,b)
C6L	19939	19487	151	17.4	Nonessential Acidic (4.8)	Perkus, *et al.* (1990a) Kotwal and Moss (1988b); Perkus, *et al.* (1990b)
C5L	20680	20069	204	24.5	Nonessential Acidic (4.8))	Kotwal and Moss (1988b); Perkus, *et al.* (1990b)
C4L	21693	20746	316	37.2	Nonessential C4B binding protein homolog; virokine	Kotwal and Moss (1988b); Perkus, *et al.* (1990b)
C3L	22551	21763	263	28.6	Nonessential	Kotwal and Moss (1988a,b); Perkus, *et al.* (1990b)
C2L	24156	22621	512	59.2	Nonessential Hydrophobic N-terminus	Kotwal and Moss (1988a) Kotwal and Moss (1988b); Perkus, *et al.* (1990b)
C1L	24900	24229	224	26.4	Nonessential Basic (9.0)	Kotwal and Moss (1988b); Perkus, *et al.* (1990b)

Reprinted from *Virology*, Vol. 179, S. J. Goebel, G. P. Johnson, M. E. Perkus, S. W. Davis, J. P. Winslow and E. Paoletti, "The Complete DNA Sequence of Vaccinia Virus", pgs. 247-266 (1990), with permission from Elsevier.

TABLE 1—*Continued*

Gene[a]	Translation Start	Translation Stop[b]	Size aa	Size M_r[c]	Characteristics	References
N1L	25240	24890	117	14.0	Nonessential	Kotwal and Moss (1988b); Perkus, *et al.* (1990b)
					Virokine	Kotwal and Moss (1988a)
					Acidic (4.2)	
N2L	25886	25362	175	20.8	Nonessential	Kotwal and Moss (1988a,b); Perkus, *et al.* (1990b)
M1L	27346	25931	472	54.2	Nonessential	Perkus, *et al.* (1990b)
					Homology to K1L	Perkus, *et al.* (1990a)
M2L	27986	27327	220	25.1	Nonessential	Perkus, *et al.* (1990b)
					Hydrophobic N-terminus	
K1L	28975	28124	284	32.6	**Host range function**	Gillard, *et al.* (1986); Perkus, *et al.* (1989)
					Nonessential	Perkus, *et al.* (1990b)
K2L	30313	29207	369	42.3	Serine protease inhibitor	Boursnell, *et al.* (1988)
					Nonessential	Perkus, *et al.* (1990b)
					Basic (9.3)	
K3L	30629	30366	88	10.5	Nonessential	Perkus, *et al.* (1990b)
					Basic (9.3)	
					Translation initiation factor	
K4L	31955	30684	424	48.9	Homology to F13L	Boursnell, *et al.* (1988)
					Nonessential	Perkus, *et al.* (1990b)
K5L	32497	32090	136	15.2	Nonessential	Perkus, *et al.* (1990b)
					Basic (10.2)	
K6L	32764	32522	81	9.1	Nonessential	Perkus, *et al.* (1990b)
K7R	32903	33349	149	17.5	Nonessential	Perkus, *et al.* (1990b)
					Acidic (4.4)	
					Hydrophobic C-terminus	
F1L	34097	33420	226	26.4	Nonessential	Perkus, *et al.* (1990b)
					Acidic (4.4)	
					Hydrophobic C-terminus	
F2L	34552	34112	147	16.3	Retroviral protease	Slabaugh and Roseman (1989)
					Nonessential	Perkus, *et al.* (1990b)
					dUTPase	
F3L	36018	34579	480	55.7	Nonessential	Perkus, *et al.* (1990b)
F4L	36988	36032	319	37.0	**Ribonucleotide reductase (small subunit)**	Slabaugh, *et al.* (1988)
					Nonessential	Perkus, *et al.* (1990b)
					Acidic (4.6)	
F5L	37985	37023	321	36.5	Multiply hydrophobic	
F6L	38239	38018	74	8.6	Acidic (4.1)	
F7L	38533	38258	92	11.0	- $(Lys-Asn)_9$	
F8L	38878	38684	65	7.8	Basic (9.9)	
F9L	39576	38941	212	23.8	Hydrophobic C-terminus	
F10L	40882	39566	439	52.2	Protein kinase 2nd signature	
F11L	41969	40908	354	39.7	-	
F12L	43919	42015	635	73.2	-	
F13L	45079	43964	372	41.8	**Envelope antigen**	Hirt, *et al.* (1986)
F14L	45318	45100	73	8.3	Acidic (2.9)	
F15L	46068	45595	159	18.6	Basic (9.5)	
F16L	46770	46078	231	26.6	Basic (9.6)	
F17R	46833	47135	101	11.3	Basic (9.8)	
E1L	48574	47138	479	55.6	-	
E2L	50784	48574	737	85.9	-	
E3L	51483	50914	190	21.5	Acidic (4.9)	
E4L	52318	51542	259	29.8	Acidic (4.9)	
					Transcription factor	

TABLE 1—*Continued*

Gene[a]	Translation Start	Translation Stop[b]	Size aa	Size M_r[c]	Characteristics	References
					(*ts*: C19??)[f]	Condit, *et al.* (1983)
E5R	52395	53387	331	39.1	Basic (9.8)	
E6R	53527	55227	567	66.7	-	
E7R	55314	55811	166	19.5	-	
E8R	55939	56757	273	31.9	Basic (9.3)	
E9L	59787	56770	1006	117.0	**DNA Polymerase** *ts*: C42, NG26; PAA^r, Aphidicolin^r DNA polymerase family B signature	Earl, *et al.*, 1986 Traktman, *et al.* (1989b)
E10R	59819	60103	95	10.8	-	
E11L	60490	60104	129	14.9	-	
O1L	62477	60480	666	77.6	Leucine Zipper Motif	
O2L	62851	62528	108	12.4	*Glutaredoxin*	
I1L	63935	63000	312	35.8	-	
I2L	64163	63945	73	8.4	Hydrophobic C-terminus Acidic (3.9)	
I3L	64973	64167	269	30.0	-	
I4L	67371	65059	771	87.0	**Ribonucleotide reductase (large subunit)** Nonessential Divalent Fe-S ferredoxin binding region signature	Schmitt and Stunnenberg (1988) Tengelsen, *et al.* (1988) Perkus, *et al.* (unpublished) Child, *et al.*, (1990)
I5L	67637	67401	79	8.7	Basic (9.9)	
I6L	68804	67659	382	43.4	Basic (9.2)	
I7L	70068	68800	423	49.0	-	
I8R	70074	72101	676	77.6	ATP/GTP binding motif A	
G1L	73883	72111	591	67.9	-	
G2R	74209	74868	220	25.7	-	
G3L	74215	73883	111	12.8	Hydrophobic N-terminus	
G4L	75215	74844	124	14.0	Acidic (4.8)	
G5R	75218	76519	434	49.9	Acidic (4.8)	
G6R	76723	77217	165	18.9	-	
G7L	78300	77188	371	41.9	-	
G8R	78331	79110	260	29.9	-	
G9R	79133	80152	340	38.8	Hydrophobic C-terminus	
L1R	80156	80905	250	27.3	Hydrophobic near C-terminus	
L2R	80940	81200	87	10.2	-	
L3L	82245	81196	350	40.6	Multiply hydrophobic	
L4R	82270	83022	251	28.5	**Structural protein, VP8**	Yang, *et al.* (1988)
L5R	83035	83418	128	14.0	Basic (10.0)	
J1R	83378	83836	153	17.8	-	
J2R	83855	84385	177	20.1	**Thymidine kinase** Nonessential ATP/GTP binding motif A	Weir and Moss (1983); Hruby *et al.* (1983) Mackett, *et al.* (1982)
J3R	84454	85452	333	15.2	Basic (10.0)	
J4R	85370	85924	185	21.3	**RNA Polymerase subunit** *ts*: C7, C20	Broyles and Moss (1986) Hooda-Dhingra, *et al.* (1989); Thompson, *et al.* (1989)
J5L	86403	86005	133	15.2	Hydrophobic C-terminus	
J6R	86510	90367	1286	146.8	**RNA Polymerase subunit** *ts*: E8, E13, E72 C51, C53, C65	Broyles and Moss (1986) Ensinger (1987) Hooda-Dhingra, *et al.*, (1989); Thompson, *et*

TABLE 1—*Continued*

Gene[a]	Translation Start	Translation Stop[b]	Size aa	Size M_r[c]	Characteristics	References
H1L	90882	90370	171	19.7	Basic (9.6)	
H2R	90896	91462	189	21.5	Hydrophobic N-terminus	
H3L	92442	91471	324	37.5	Multiply hydrophobic	
H4L	94830	92446	795	93.6	-	
H5R	95016	95624	203	22.3	-	
H6R	95628	96569	314	36.7	Basic (10.0)	
H7R	96609	97046	146	16.9	DNA topoisomerase -	Shuman and Moss (1987)
D1R	97093	99624	844	96.7	mRNA capping enzyme (small subunit)	Morgan, *et al.* (1984)
D2L	100026	99589	146	16.9	*ts*: E52, E94	Seto, *et al.* (1987)
D3R	100019	100729	237	28.0	*ts*: C5, C35	Seto, *et al.* (1987)
D4R	100732	101385	218	25.0	-	
D5R	101420	103774	785	90.0	*ts*: C17, C24, E69 ATP/GTP binding motif A	Seto, *et al.* (1987)
D6R	103818	105728	637	73.8	Early transcription factor subunit *ts*: C46, E93 Hydrophobic N-terminus	Broyles and Fesler (1990) Seto, *et al.* (1987)
D7R	105758	106240	161	17.9	RNA polymerase subunit *ts*: C21, E45 Acidic (4.5)	Ahn, *et al.* (1990) Seto, *et al.* (1987)
D8L	107120	106209	304	35.3	Carbonic anhydrase Transmembrane Cell surface binding Multiply hydrophobic Basic (9.1)	Niles, *et al.* (1986) Niles and Seto (1988) Maa, *et al* (1990)
D9R	107162	107800	213	25.0	-	
D10R	107800	108543	248	28.9	-	
D11L	110442	108550	631	72.4	NTPase *ts*: C36, C50, E17 Basic (9.0)	Rodriguez, *et al.* (1986); Broyles and Moss (1987) Seto, *et al.* (1987)
D12L	111340	110480	287	33.4	mRNA capping enzyme (small subunit)	Niles, *et al.* (1989)
D13L	113026	111374	551	61.9	*ts*: C33, C43, E101 Rifampicin resistance Acidic (5.0)	Seto, *et al.* (1987) Tartaglia and Paoletti (1985); Baldick and Moss (1987)
A1L	113502	113053	150	17.0	-	
A2L	114197	113526	224	26.3	-	
A3L	116372	114441	644	72.6	Major core protein P4b	Rosel and Moss (1985)
A4L	117270	116428	281	30.8	Acidic (4.6)	
A5R	117308	117799	164	19.0	Acidic (4.2)	
A6L	118917	117802	372	43.1	-	
A7L	121073	118944	710	82.3	Early transcription factor subunit	Gershon and Moss (1990)
A8R	121127	121990	288	33.6	-	
A9L	122285	121989	99	11.1	-	
A10L	124961	122289	891	102.3	Major core protein P4a	Van Meir and Wittek (1988)
A11R	124976	125929	318	36.1	Hydrophobic C-terminus Acidic (4.7)	
A12L	126512	125937	192	20.5	Basic (10.1)	
A13L	126748	126539	70	7.7	Basic (9.7)	
A14L	127128	126859	90	10.0	-	
A15L	127580	127299	94	11.0	-	
A16L	128700	127567	378	43.6	Hydrophobic C-terminus	
A17L	129314	128706	203	23.0	Hydrophobic center Acidic (4.1)	
A18R	129329	130807	493	56.7	Basic (9.3)	

TABLE 1—*Continued*

Gene[a]	Translation Start	Translation Stop[b]	Size aa	Size M_r[c]	Characteristics	References
A19L	131024	130794	77	8.3	–	
A20R	131377	132654	426	49.2	–	
A21L	131378	131028	117	13.6	Hydrophobic N-terminus	
A22R	132620	133147	176	20.7	Basic (9.9)	
A23R	133170	134315	382	44.6	–	
A24R	134315	137806	1164	133.4	**RNA polymerase subunit;** *ts*: C27, C29, C32, C47, C62	Hooda-Dhingra, *et al.* (1990) Hooda-Dhingra, *et al*, (1990)
					Leucine Zipper Pattern	
A25L	138011	137817	65	7.5	A-type inclusion protein (cowpox virus)	Funahashi, *et al.* (1988);
					Acidic (3.3)	
A26L	138948	137983	322	37.3	A-type Inclusion protein (cowpox virus)	Funahashi, *et al.* (1988);
					Basic (9.2)	
A27L	139330	139001	110	12.6	**Fusion protein**	Rodriguez & Esteban (1987)
A28L	139771	139334	146	16.3	–	
A29L	140689	139775	305	35.4	–	
A30L	140885	140655	77	8.7	Basic (9.9)	
A31R	141045	141416	124	14.2	Basic (9.0)	
					Ribonucleoprotein RNA-binding region signature	
A32L	142288	141389	300	34.4	Basic (9.2)	
					ATP/GTP Binding motif A	
A33R	142316	142870	185	20.5	–	
A34R	142897	143400	168	19.5	Basic (10.1)	
A35R	143447	143974	176	20.0	Acidic (4.0)	
A36R	144044	144706	221	25.1	Acidic (4.4)	
A37R	144773	145561	263	29.9	–	
A38L	146678	145848	277	31.6	Multiply hydrophobic	
A39R	146695	147903	403	45.7	–	
A40R	147932	148435	168	19.3	Hydrophobic N-terminus	
A41L	149155	148499	219	25.1	Acidic (4.8)	
A42R	149334	149732	133	15.0	Basic (9.9)	
					Profilin	
A43R	149773	150354	194	22.6	–	
A44L	151733	150696	346	39.4	*3ß-Hydroxy-5-ene steroid dehydrogenase*	
A45R	151780	152154	125	13.8	*Superoxide dismutase*	
A46R	152147	152788	214	24.7	–	
A47L	153690	152959	244	28.3	Basic (10.0)	
A48R	153789	154400	204	23.2	**Thymidylate kinase**	Smith, *et al.* (1989a)
					ATP/GTP binding motif A	
					Acidic (5.0)	
A49R	154451	154936	162	18.8	Acidic (3.9)	
A50R	154972	156627	552	63.4	**DNA Ligase**	Colinas, *et al.* (1990); Smith, *et al.* (1989a); Kerr and Smith (1989)
					Nonessential	Colinas, *et al.* (1990)
A51R	156683	157684	334	37.7	Nonessential	Davis, *et al.* (unpublished)
A52R	157757	158326	190	22.7	Hydrophilic N-terminus	
A53R	158635	158943	103	12.0	Nonessential	Davis, *et al.* (unpublished)
A54L	158743	158474	90	10.8	Basic (10.4)	
					Nonessential	Davis, *et al.* (unpublished)
A55R	159442	161133	564	64.7	Nonessential	Davis, *et al.* (unpublished)
A56R	161186	162130	315	34.8	Nonessential	Shida, *et al.* (1987)
					Hemagglutinin	Shida (1986)
					Hydrophobic C-terminus	
					Acidic (3.9)	
A57R	162278	162730	151	17.4	–	

TABLE 1—*Continued*

Gene[a]	Translation Start	Translation Stop[b]	Size aa	Size M_r[c]	Characteristics	References
B1R	162884	163783	300	34.3	*ts*: C2, C3, C25 Protein Kinase Basic (9.1)	Traktman, *et al.* (1989a) Howard and Smith (1989)
B2R	163876	164532	219	24.6	-	
B3R	164571	164942	124	14.4	Acidic (4.7)	
B4R	165603	167276	558	65.3	-	
B5R	167383	168333	317	35.1	Multiply hydrophobic Acidic (4.4) *Complement control proteins* *C3L homologue*	
B6R	168432	168950	173	20.1	-	
B7R	168991	169536	182	21.3	Hydrophobic N-terminus	
B8R	169594	170409	272	31.2	Hydrophobic N-terminus	
B9R	170499	170729	77	8.8	-	
B10R	170695	171192	166	18.9	-	
B11R	171267	171530	88	9.9	Acidic (3.6) M(DT)$_9$DVTNV...	
B12R	171600	172448	283	33.4	Protein Kinase	Howard and Smith (1989)
B13R	172562	172909	116	12.8	Hemorrhage-inducing Serine Protease Inhibitor Nonessential Acidic (4.6)	Pickup, *et al.* (1986) Kotwal and Moss (1989); Perkus, *et al.* (1990b)
B14R	172887	173552	222	24.9	Hemorrhage-inducing Serine Protease Inhibitor Nonessential Acidic (4.3)	Pickup, *et al.* (1986) Kotwal and Moss (1989) Perkus, *et al.* (1990b)
B15R	173632	174078	149	17.4	Nonessential Acidic (4.5)	Perkus, *et al.* (1990b)
B16R	174272	175141	290	32.5	Nonessential *Kinase-related transforming protein*	Perkus, *et al.* (1990b)
B17L	176212	175193	340	39.5	Nonessential	Perkus, *et al.* (1990b)
B18R	176349	178070	574	68.1	Nonessential	Perkus, *et al.* (1990b)
B19R	178145	179203	353	40.9	Hydrophobic N-terminus Nonessential	Perkus, *et al.* (1990b)
B20R	179300	179680	127	15.5	Nonessential Acidic (4.1)	Perkus, *et al.* (1990b)
B21R*	180585	180857	91	10.5	Nonessential; C15L	Perkus, *et al.* (1990b)
B22R*	181199	181741	181	21.0	Nonessential; C16L	Perkus, *et al.* (1990b)
B23R*	181791	182948	386	44.9	Nonessential; C17L	Perkus, *et al.* (1990b)
B24R*	183045	183494	150	17.5	Nonessential; C18L Acidic (4.8)	Perkus, *et al.* (1990b)
B25R*	183882	184658	259	30.5	Hydrophobic N-terminus Nonessential; C19L	Perkus, *et al.* (1990b)
B26R*	184606	184914	103	12.5	Nonessential; C20L Basic (9.0)	Perkus, *et al.* (1990b)
B27R*	184923	185261	113	13.4	Nonessential; C21L	Perkus, *et al.* (1990b)
B28R*	185625	185990	122	13.6	Nonessential; C22L Hydrophobic N-terminus	Perkus, *et al.* (1990b)
B29R*	186730	187461	244	26.4	Nonessential; C23L Acidic (4.2)	Perkus, *et al.* (1990b)

[a] Open reading frames enumerated as described in text.

[b] Translation stop does not incude the three bases of termination codon.

[c] M_r values calculated for the nascent, unprocessed polypeptide chain are presented as kDa.

[d] Functions or activities indicated in bold type are known functions of vaccinia virus. Those indicated in *italics* have been identified in this study on the basis of similarity to existing proteins. All others are possible functions previously described by other investigators.

[e] Acidic proteins: p*I* < 5.0; basic proteins: p*I* > 9.0. p*I* presented within parentheses.

[f] Temperature-sensitive mutants indicated by *ts*. Those first isolated by Condit *et al.* (1983) are prefaced with C; t
begin with E. Mutant C19, while not localized to a particular open reading frame, appears to map in the vincinity of I

* Open reading frames repeated in both left and right termini of genome.

REFERENCES

AHN, B.-Y., JONES, E. V., and Moss, B. (1990). Identification of the vaccinia virus gene encoding an 18-kilodalton subunit of RNA polymerase and demonstration of a 5' poly(A) leader on its early transcript. *J. Virol.* 64, 3019–3024.

BAIROCH, A. (1989). "PROSITE: A Dictionary of Protein Sites and Patterns," 2nd ed. University of Geneva, Geneva.

BALDICK, C. J., JR., and Moss, B. (1987). Resistance of vaccinia virus to rifampicin conferred by a single nucleotide substitution near the predicted NH_2 terminus of a gene encoding an *M*, 62,000 polypeptide. *Virology* 156, 138–145.

BAROUDY, B. M., and Moss, B. (1982). Sequence homologies of diverse length tandem repetitions near ends of vaccinia virus genome suggest unequal crossing over. *Nucleic Acids Res.* 10, 5673–5679.

BAROUDY, B. M., VENKATESAN, S., and Moss, B. (1982). Incompletely base-paired flip-flop terminal loops link the two DNA strands of the vaccinia virus genome into one uninterrupted polynucleotide chain. *Cell* 28, 315–324.

BAUSE, E. (1983). Structural requirements of N-glycosylation of proteins: Studies with proline peptides as conformational probes. *Biochem. J.* 209, 331–336.

BLOMQUIST, M. C., HUNT, L. T., and BARKER, W. C. (1984). Vaccinia virus 19-kilodalton protein: Relationship to several mammalian proteins, including two growth factors. *Proc. Natl. Acad. Sci. USA* 81, 7363–7367.

BOURSNELL, M. E. G., FOULDS, I. J., CAMPBELL, J. I., and BINNS, M. M. (1988). Nonessential genes in the vaccinia virus *Hin*dIII K fragment: A gene related to serine protease inhibitors and a gene related to the 37K vaccinia virus major envelope antigen. *J. Gen. Virol.* 69, 2995–3003.

BROWN, J. P., TWARDZIK, D. R., MARQUARDT, H., and TODARO, G. J. (1985). Vaccinia virus encodes a polypeptide homologous to epidermal growth factor and transforming growth factor. *Nature (London)* 313, 491–492.

BROYLES, S. S., and FESLER, B. S. (1990). Vaccinia virus gene encoding a component of the viral early transcription factor. *J. Virol.* 64, 1523–1529.

BROYLES, S. S., and Moss, B. (1986). Homology between RNA polymerases of poxviruses, prokaryotes, and eukaryotes: Nucleotide sequence and transcriptional analysis of vaccinia virus genes encoding 147-kDa and 22-kDa subunits. *Proc. Natl. Acad. Sci. USA* 83, 3141–3145.

BROYLES, S. S., and Moss, B. (1987). Identification of the vaccinia virus gene encoding nucleoside triphosphate phosphohydrolase I, a DNA-dependent ATPase. *J. Virol.* 61, 1738–1742.

BULLER, M. L., CHAKRABARTI, S., COOPER, J. A., TWARDZIK, D. R., and Moss, B. (1988). Deletion of the vaccinia virus growth factor gene reduces virus virulence. *J. Virol.* 62, 866–874.

CHILD, S. J., PALUMBO, G. J., BULLER, R. M. L., and HRUBY, D. E. (1990). Insertional inactivation of the large subunit of ribonucleotide reductase encoded by vaccinia virus is associated with reduced virulence *in vivo*. *Virology* 174, 625–629.

COLINAS, R. J., GOEBEL, S. J., DAVIS, S. W., JOHNSON, G. P., NORTON, E. K., and PAOLETTI, E. (1990). A DNA ligase gene in the Copenhagen strain of vaccinia virus is nonessential for viral replication and recombination. *Virology* 179, 267–275.

CONDIT, R. C., MOTYCZKA, A., and SPIZZ, G. (1983). Isolation, characterization and physical mapping of temperature-sensitive mutants of vaccinia virus. *Virology* 128, 429–443.

DAVISON, A. J., and Moss, B. (1989). Structure of vaccinia virus late promoters. *J. Mol. Biol.* 210, 771–784.

DEFILIPPES, F. M. (1982). Restriction enzyme mapping of vaccinia virus DNA. *J. Virol.* 43, 136–149.

EARL, P. L., JONES, E. V., and Moss, B. (1986). Homology between DNA polymerase of poxviruses, herpesviruses, and adenoviruses: Nucleotide sequence of the vaccinia virus DNA polymerase gene. *Proc. Natl. Acad. Sci. USA* 83, 3659–3663.

EARL, P. L., and Moss, B. (1987). Vaccinia virus. *In* "Genetic Maps" (S. J. O'Brien, Ed.), Vol. 4, pp. 116–123. Cold Spring Harbor Laboratory, Cold Spring Harbor, NY.

EISENBERG, D., SCHWARZ, E., KOMAROMY, M., and WALL, R. (1984). Analysis of membrane and surface protein sequences with the hydrophobic moment plot. *J. Mol. Biol.* 179, 125–142.

ENSINGER, M. J. (1982). Isolation and genetic characterization of temperature-sensitive mutants of vaccinia virus WR. *J. Virol.* 43, 778–790.

ENSINGER, M. J. (1987). Phenotypic characterization of temperature-sensitive mutants of vaccinia virus with mutations in a 135,000-*M*, subunit of the virion-associated DNA-dependent RNA polymerase. *J. Virol.* 61, 1842–1850.

ERNST, H., DUNCAN, R. F., and HERSHEY, J. W. B. (1987). Cloning and sequencing of complementary DNAs encoding the α-subunit of translational initiation factor eIF-2: Characterization of the protein and its messenger RNA. *J. Biol. Chem.* 262, 1206–1212.

FRANKE, C. A., REYNOLDS, P. L., and HRUBY, D. E. (1989). Fatty acid acylation of vaccinia virus proteins. *J. Virol.* 63, 4285–4291.

FUNAHASHI, S., SATO, T., and SHIDA, H. (1988). Cloning and characterization of the gene encoding the major protein of the A-type inclusion body of cowpox virus. *J. Gen. Virol.* 69, 35–47.

GARON, C. F., BARBOSA, E., and Moss, B. (1978). Visualization of an inverted terminal repetition in vaccinia virus DNA. *Proc. Natl. Acad. Sci. USA* 75, 4863–4867.

GERSHON, P. D., and Moss, B. (1990). Early transcription factor subunits are encoded by vaccinia virus late genes. *Proc. Natl. Acad. Sci. USA* 87, 4401–4405.

GILLARD, S., SPEHNER, D., DRILLIEN, R., and KIRN, A. (1986). Localization and sequence of a vaccinia virus gene required for multiplication in human cells. *Proc. Natl. Acad. Sci. USA* 83, 5573–5577.

GUO, P., GOEBEL, S., DAVIS, S., PERKUS, M. E., LANGUET, B., DESMETTRE, P., ALLEN, G., and PAOLETTI, E. (1989). Expression in recombinant vaccinia virus of the equine herpesvirus 1 gene encoding glycoprotein gp13 and protection of immunized animals. *J. Virol.* 63, 4189–4198.

HANGGI, M., BANNWARTH, W., and STUNNENBERG, H. G. (1986). Conserved TAAAT motif in vaccinia virus late promoters: Overlapping TATA box and site of transcription initiation. *EMBO J.* 5, 1071–1076.

HATTORI, M., and SAKAKI, Y. (1986). Dideoxy sequencing method using denatured plasmid templates. *Anal. Biochem.* 152, 232–237.

HIRASHIMA, S., HIRAI, H., NAKANISHI, Y., and NATORI, S. (1988). Molecular cloning and characterization of cDNA for eukaryotic transcription factor S-II. *J. Biol. Chem.* 263, 3858–3863.

HIRT, P., HILLER, G., and WITTEK, R. (1986). Localization and fine structure of a vaccinia virus gene encoding an envelope antigen. *J. Virol.* 58, 757–764.

HOODA-DHINGRA, U., THOMPSON, C. L., and CONDIT, R. C. (1989). Detailed phenotypic characterization of five temperature-sensitive mutants in the 22- and 147-kilodalton subunits of vaccinia virus DNA-dependent RNA polymerase. *J. Virol.* 63, 714–729.

HOODA-DHINGRA, U., PATEL, D. D., PICKU
(1990). Fine structure mapping and f

temperature-sensitive mutations in the second largest subunit of vaccinia virus DNA-dependent RNA polymerase. *Virology* 174, 60–69.

HOWARD, S. T., and SMITH, G. L. (1989). Two early vaccinia virus genes encode polypeptides related to protein kinases. *J. Gen Virol.* 70, 3187–3201.

HRUBY, D. E., MAKI, R. A., MILLER, D. B., and BALL, L. A. (1983). Fine structure analysis and nucleotide sequence of the vaccinia virus thymidine kinase gene. *Proc. Natl. Acad. Sci. USA* 80, 3411–3415.

KERR, S. M., and SMITH, G. L. (1989). Vaccinia virus encodes a polypeptide with DNA ligase activity. *Nucleic Acids Res.* 17, 9039–9050.

KLEIN, P., KANEHISA, M., and DELISI, C. (1985). The detection and classification of membrane-spanning proteins. *Biochem. Biophys. Acta* 815, 468–476.

KLINTROT, I.-M., HOOG, J.-O., JORNVALL, H., HOLMGREN, A., and LUTHMAN, M. (1984). The primary structure of calf thymus glutaredoxin: Homology with the corresponding *Escherichia coli* protein but elongation at both ends and with an additional half-cystine/cysteine pair. *Eur. J. Biochem.* 144, 417–423.

KOTWAL, G. J., and MOSS, B. (1988a). Vaccinia virus encodes a secretory polypeptide structurally related to complement control proteins. *Nature (London)* 335, 176–178.

KOTWAL, G. J., and MOSS, B. (1988b). Analysis of a large cluster of nonessential genes deleted from a vaccinia virus terminal transposition mutant. *Virology* 167, 524–537.

KOTWAL, G. J., and MOSS, B. (1989). Vaccinia virus encodes two proteins that are structurally related to members of the plasma serine protease inhibitor superfamily. *J. Virol.* 63, 600–606.

KOZAK, M. (1986). Point mutations define a sequence flanking the AUG initiator codon that modulates translation by eukaryotic ribosomes. *Cell* 44, 283–292.

KWIATKOWSKI, D. J., and BRUNS, G. A. P. (1988). Human profilin: Molecular cloning, sequence comparison, and chromosomal analysis. *J. Biol. Chem.* 263, 5910–5915.

KYTE, J., and DOOLITTLE, R. F. (1982). A simple method for displaying the hydropathic character of a protein. *J. Mol. Biol.* 157, 105–132.

LIPMAN, D. J., and PEARSON, W. R. (1985). Rapid and sensitive protein similarity searches. *Science* 227, 1435–1441.

LUNDBERG, L. G., THORESSON, H.-O., KARLSTROM, O. H., and NYMAN, P. O. (1983). Nucleotide sequence of the structural gene for dUTPase of *Escherichia coli* K-12. *EMBO J.* 2, 967–971.

LUU, T. V., LACHANCE, Y., LABRIE, C., LEBLANC, G., THOMAS, J. L., STRICKLER, R. C., and LABRIE, F. (1989). Full length cDNA structure and deduced amino acid sequence of human 3β-hydroxy-5-ene steroid dehydrogenase. *Mol. Endocrinol.* 3, 1310–1312.

LUX, S. E., JOHN, K. M., and BENNETT, V. (1990). Analysis of cDNA for human erythrocyte ankyrin indicates a repeated structure with homology to tissue-differentiation and cell-cycle control proteins. *Nature (London)* 334, 36–42.

MAA, J.-S., RODRIGUEZ, J. F., and ESTEBAN, M. (1990). Structural and functional characterization of a cell surface binding protein of vaccinia virus. *J. Biol. Chem.* 265, 1569–1577.

MACKETT, M., and ARCHARD, L. C. (1979). Conservation and variation in *Orthopoxvirus* genome structure. *J. Gen. Virol.* 45, 683–701.

MACKETT, M., SMITH, G. L., and MOSS, B. (1982). Vaccinia virus: A selectable eukaryotic cloning and expression vector. *Proc. Natl. Acad. Sci. USA* 79, 7415–7419.

MAXAM, A. M., and GILBERT, W. (1980). Sequencing end-labeled DNA with base-specific chemical cleavages. *In* "Methods in Enzymology" (L. Grossman and K. Moldave, Eds.), Vol. 65, pp. 499–560. Academic Press, New York.

MERCHLINSKY, M., and MOSS, B. (1989). Nucleotide sequence required for resolution of the concatemer junction of vaccinia virus DNA. *J. Virol.* 63, 4354–4361.

MORGAN, J. R., COHEN, L. K., and ROBERTS, B. E. (1984). Identification of the DNA sequence encoding the large subunit of the mRNA-capping enzyme of vaccinia virus. *J. Virol.* 52, 206–214.

MOSS, B. (1985). Replication of poxviruses. *In* "Virology" (B. Fields, R. M. Chanock, and B. Roizman, Eds.), pp. 685–703. Raven Press, New York.

MOSS, B. (1990). Poxviridae and their replication. *In* "Virology" (B. N. Fields *et al.*, Eds.), 2nd ed., pp. 2079–2111. Raven Press, New York.

MOSS, B., WINTERS, E., and COOPER, N. (1981). Instability and reiteration of DNA sequences within the vaccinia virus genome. *Proc. Natl. Acad. Sci. USA* 78, 1614–1618.

NILES, E. G., CONDIT, R. C., CARO, P., DAVIDSON, K., MATUSICK, L., and SETO, J. (1986). Nucleotide sequence and genetic map of the 16-kb vaccinia virus *Hin*dIII D fragment. *Virology* 153, 96–112.

NILES, E. G., LEE-CHEN, G.-J., SHUMAN, S., MOSS, B., and BROYLES, S. S. (1989). Vaccinia virus gene D12L encodes the small subunit of the viral mRNA capping enzyme. *Virology* 172, 513–522.

NILES, E. G., and SETO, J. (1988). Vaccinia virus gene D8 encodes a virion transmembrane protein. *J. Virol.* 62, 3772–3778.

NYSTROM, L.-E., LINDBERG, U., KENDRICK-JONES, J., and JAKES, R. (1979). The amino acid sequence of profilin from calf spleen. *FEBS Lett.* 101, 161–165.

PANICALI, D., and PAOLETTI, E. (1982). Construction of poxviruses as cloning vectors: Insertion of the thymidine kinase gene from herpes simplex virus into the DNA of infectious vaccinia virus. *Proc. Natl. Acad. Sci. USA* 79, 4927–4931.

PATEL, D. D., RAY, C. A., DRUCKER, R. P., and PICKUP, D. J. (1988). A poxvirus-derived vector that directs high levels of expression of cloned genes in mammalian cells. *Proc. Natl. Acad. Sci. USA* 85, 9431–9435.

PERKUS, M. E., GOEBEL, S. J., DAVIS, S. W., JOHNSON, G. P., LIMBACH, K., NORTON, E. K., and PAOLETTI, E. (1990a). Vaccinia virus host range genes. *Virology* 179, 276–286.

PERKUS, M. E., GOEBEL, S. J., DAVIS, S. W., JOHNSON, G. P., NORTON, E. K., and PAOLETTI, E. (1990b). Deletion of fifty five open reading frames from the termini of vaccinia virus. *Virology*, in press.

PERKUS, M. E., LIMBACH, K., and PAOLETTI, E. (1989). Cloning and expression of foreign genes in vaccinia virus, using a host range selection system. *J. Virol.* 63, 3829–3836.

PICKUP, D. J., INK, B. S., HU, W., RAY, C. A., and JOKLIK, W. K. (1986). Hemorrhage in lesions caused by cowpox virus is induced by a viral protein that is related to plasma protein inhibitors of serine proteases. *Proc. Natl. Acad. Sci. USA* 83, 7698–7702.

PLUCIENNICZAK, A., SCHROEDER, E., ZETTLENEISSEL, G., and STRECK, R. E. (1985). Nucleotide sequence of a cluster of early and late genes in a conserved segment of the vaccinia virus genome. *Nucleic Acids Res.* 13, 985–998.

RAO, J. K. M., and ARGOS, P. (1986). A conformational preference parameter to predict helices in integral membrane proteins. *Biochem. Biophys. Acta* 869, 197–214.

REISNER, A. H. (1985). Similarity between the vaccinia virus 19K early protein and epidermal growth factor. *Nature (London)* 313, 801–803.

RODRIGUEZ, J. F., and ESTEBAN, M. (1987). Mapping and nucleotide sequence of the vaccinia virus gene that encodes a 14-kilodalton fusion protein. *J. Virol.* 61, 3550–3554.

RODRIGUEZ, J. F., KAHN, J. S., and ESTEBAN, M. (1986). Molecular cloning, encoding sequence, and expression of vaccinia virus nucleic acid-dependent nucleoside triphosphatase gene. *Proc. Natl. Acad. Sci. USA* 83, 9566–9570.

ROSEL, J. L., EARL, P. L., WEIR, J. P., and MO

TAAATG sequence at the transcriptional and translational initiation sites of vaccinia virus late genes deduced by structural and functional analysis of the *Hin*dIII H genomic fragment. *J. Virol.* 60, 436–449.

ROSEL, J. L., and MOSS, B. (1985). Transcriptional and translational mapping and nucleotide sequence analysis of a vaccinia virus gene encoding the precursor of the major core polypeptide 4b. *J. Virol.* 56, 830–838.

SCHMITT, J. F. C., and STUNNENBERG, H. G. (1988). Sequence and transcriptional analysis of the vaccinia virus *Hin*dIII I fragment. *J. Virol.* 62, 1889–1897.

SETO, J., CELENZA, L. M., CONDIT, R. C., and NILES, E. G. (1987). Genetic map of the vaccinia virus *Hin*dIII D fragment. *Virology* 160, 110–119.

SHIDA, H. (1986). Nucleotide sequence of the vaccinia virus hemagglutinin gene. *Virology* 150, 451–462.

SHIDA, H., TOCHIKURA, T., SATO, T., KONNO, T., HIRAYOSHI, K., SEKI, M., ITO, Y., HATANAKA, M., HINUMA, Y., SUGIMOTO, M., TAKAHASHI-NISHIMAKI, F., MARUYAMA, T., MIKI, K., SUZUKI, K., MORITA, M., SASHIYAMA, H., and HAYAMI, M. (1987). Effect of the recombinant vaccinia viruses that express HTLV-I envelope gene on HTLV-I infection. *EMBO J.* 6, 3379–3384.

SHUMAN, S., and MOSS, B. (1987). Identification of a vaccinia virus gene encoding a type I DNA topoisomerase. *Proc. Natl. Acad. Sci. USA* 84, 7478–7482.

SLABAUGH, M. B., and ROSEMAN, N. A. (1989). Retroviral protease-like gene in the vaccinia virus genome. *Proc. Natl. Acad. Sci. USA* 86, 4152–4155.

SLABAUGH, M. B., ROSEMAN, N., DAVIS, R., and MATTHEWS, C. (1988). Vaccinia virus-encoded ribonucleotide reductase: Sequence conservation of the gene for the small subunit and its amplification in hydroxyurea-resistant mutants. *J. Virol.* 62, 519–527.

SMITH, G. L., CHAN, Y. S., and KERR, S. M. (1989a). Transcriptional mapping and nucleotide sequence of a vaccinia virus gene encoding a polypeptide with extensive homology to DNA ligases. *Nucleic Acids Res.* 17, 9051–9062.

SMITH, G. L., DECARLOS, A., and CHAN, Y. S. (1989b). Vaccinia virus encodes a thymidylate kinase gene: Sequence and transcriptional mapping. *Nucleic Acids Res.* 17, 7581–7590.

SMITH, G. L., HOWARD, S. T., and CHAN, Y. S. (1989c). Vaccinia virus encodes a family of genes with homology to serine protease inhibitors. *J. Gen. Virol.* 70, 2333–2343.

SPEHNER, D., GILLARD, S., DRILLIEN, R., and KIRN, A. (1988). A cowpox virus gene required for multiplication in chinese hamster ovary cells. *J. Virol.* 62, 1297–1304.

SRI WIDADA, J., FERRAZ, C., and LIAUTARD, J. P. (1989). Total coding sequence of profilin cDNA from *Mus musculus* macrophage. *Nucleic Acids Res.* 17, 2855.

TABOR, S., and RICHARDSON, C. C. (1987). DNA sequence analysis with a modified bacteriophage T7 polymerase. *Proc. Natl. Acad. Sci. USA* 84, 4767–4771.

TAMIN, A., VILLARREAL, E. C., WEINRICH, S. L., and HRUBY, D. E. (1988). Nucleotide sequence and molecular genetic analysis of the vaccinia virus *Hin*dIII N/M region encoding the genes responsible for resistance to alpha-amanitin. *Virology* 165, 141–150.

TARTAGLIA, J., and PAOLETTI, E. (1985). Physical mapping and DNA sequence analysis of the rifampicin resistance locus in vaccinia virus. *Virology* 147, 394–404.

TENGELSEN, L. A., SLABAUGH, M. B., BIBLER, J. K., and HRUBY, D. E. (1988). Nucleotide sequence and molecular genetic analysis of the large subunit of ribonucleotide reductase encoded by vaccinia virus. *Virology* 164, 121–131.

THOMPSON, C. L., HOODA-DHINGRA, U., and CONDIT, R. C. (1989). Fine structure mapping of five temperature-sensitive mutants in the 22- and 147-kilodalton subunits of vaccinia virus DNA-dependent RNA polymerase. *J. Virol.* 63, 705–713.

TRAKTMAN, P., ANDERSON, M. K., and REMPEL, R. E. (1989a). Vaccinia virus encodes an essential gene with strong homology to protein kinases. *J. Biol. Chem.* 264, 21,458–21,461.

TRAKTMAN, P., KELVIN, M., and PACHECO, S. (1989b). Molecular genetic analysis of vaccinia virus DNA polymerase mutants. *J. Virol.* 63, 841–846.

VAN MEIR, E., and WITTEK, R. (1988). Fine structure of the vaccinia virus gene encoding the precursor of the major core protein 4a. *Arch. Virol.* 102, 19–27.

VENKATESAN, S., BAROUDY, B. M., and MOSS, B. (1981). Distinctive nucleotide sequences adjacent to multiple initiation and termination sites of an early vaccinia virus gene. *Cell* 125, 805–813.

VENKATESAN, S., GERSHOWITZ, A., and MOSS, B. (1982). Complete nucleotide sequences of two adjacent early vaccinia virus genes located within the terminal repetition. *J. Virol.* 44, 637–646.

VON HEIJNE, G. (1986). A new method for predicting signal sequence cleavage sites. *Nucleic Acids Res.* 14, 4683–4690.

WEINRICH, S. L., and HRUBY, D. E. (1986). A tandemly-oriented late gene cluster within the vaccinia virus genome. *Nucleic Acids Res.* 14, 3003–3016.

WEIR, J. P., and MOSS, B. (1983). Nucleotide sequence of the vaccinia virus thymidine kinase gene and the nature of spontaneous frameshift mutations. *J. Virol.* 46, 530–537.

WITTEK, R., MULLER, H. K., MENNA, A., and WYLER, R. (1978). Length heterogeneity in the DNA of vaccinia virus is eliminated on cloning the virus. *FEBS Lett.* 90, 41–46.

YANG, W.-P., KAO, S.-Y., and BAUER, W. R. (1988). Biosynthesis and post-translational cleavage of vaccinia virus structural protein VP8. *Virology* 167, 585–590.

YUEN, L., and MOSS, B. (1987). Oligonucleotide sequence signalling transcriptional termination of vaccinia virus early genes. *Proc. Natl. Acad. Sci. USA* 84, 6417–6421.

TABLE 2

Features and Homologies of Open Reading Frames of the Vaccinia MVA Strain

ORF[a] START STOP	AA[b]	kDa[c]	name / (putative) function / homologies[g]	BLAST[d] expect	BLAST[e] AA id	HSS[f] (%)	references
left terminal	region:						
001L/ 6822	136	14.9	35k major secr. protein				(Patel *et al.*, 1990)
193R[h] 6412			chemokine receptor (f')				(Graham *et al.*, 1997)
C23L	244		VAC (*C23L/B29R*)	6.0e-57	41/42	97	(Goebel *et al.*, 1990)
	253		VAR-I' G3R	8.9e-51	46/49	93	(Shchelkunov *et al.*, 1995)
	246		CPX ORF B	5.6e-49	40/42	95	(Hu *et al.*, 1994)
	258		SFV T1 protein	2.5e-20	23/42	54	(Upton *et al.*, 1987)
	260		Myxoma virus T1/35kDa	1.5e-14	21/42	50	(Graham *et al.*, 1997)
002L/ 7784	176	19.7	secr. TNF receptor (f)				(Upton *et al.*, 1991a)
192R[h] 7254	355		CPX crmB	5.1e-71	76/83	91	(Hu *et al.*, 1994)
	348		VAR-BSH G2R	1.0e-66	73/83	87	(Shchelkunov *et al.*, 1995)
	326		Myxoma virus T2	4.9e-30	21/37	56	(Upton *et al.*, 1991a)
	325		Rabbit fibroma Virus T2	1.8e-28	17/36	47	(Upton *et al.*, 1987)
	202		CPX C4L	8.7e-15	30/51	58	(Safronov *et al.*, 1996)
	346		[H]S TNF receptor protein	1.9e-08	14/26	53	(Heller *et al.*, 1990)
C19L	259		VAC (*C19L/B25R*)	0.00026	16/19	84	(Goebel *et al.*, 1990)
	277		human CD40L receptor	0.0015	11/24	45	(Stamenkovic *et al.*, 1989)
			30 matches to TNF receptors and surface proteins	<0.39			
003L/ 8780	102	12.1	45k ank[k]-like protein (f1)				(Goebel *et al.*, 1990)
191R[h] 8472							
C17L	386		VAC C17L/B23R	1.3e-39	62/63	98	(Goebel *et al.*, 1990)
004L/ 9558	233	26.9	45k ank-like protein (f2)				(Goebel *et al.*, 1990)
190R[h] 8857							
C17L	386		VAC (C17L/B23R)	6.2e-159	110/110	100	(Goebel *et al.*, 1990)
D1L	91		VAR-BSH	9.1e-31	46/49	93	(Shchelkunov *et al.*, 1995)
	669		CPX host range	1.1e-13	22/50	44	(Spehner *et al.*, 1988)
	452		VAR-I D6L (BSH:D8L)	1.7e-11	21/50	42	(Shchelkunov *et al.*, 1995)
	574		VAR-I B19R (BSH: B16R)	1.2e-05	22/73	30	(Shchelkunov *et al.*, 1995)
	574		VAC B18R (WR: B17R)	8.6e-05	22/73	30	(Goebel *et al.*, 1990)
	634		VAC C9L	0.00011	11/24	45	(Kotwal and Moss, 1988a)
	585		VAR-I G1R	0.00013	22/74	29	(Shchelkunov *et al.*, 1995)
	516		orf virus	0.0088	15/49	30	(Sullivan *et al.*, 1995b)
	153		VAR-I D7L (BSH:D10L)	0.014	12/28	42	(Shchelkunov *et al.*, 1995)
005R 10203	140	15.5	Growth factor (EGF receptor binding)				(Twardzik *et al.*, 1985)
10625							(Stroobant *et al.*, 1985)
C11R	142		VAC	2.9e-82	99/104	95	(Goebel *et al.*, 1990)
D2R	140		VAR-I (BSH:D4R)	3.6e-74	106/140	75	(Shchelkunov *et al.*, 1995)
	138		CPX D5R	3.4e-95	101/114	88	(Safronov *et al.*, 1996)
	169		human epiregulin	2.2e-14	29/78	37	D30783
			100 matches to growth factor like sequences	<0.10			
006L 11758	326	37.9	37.9k protein				(Venkatesan *et al.*, 1982)
C10L 10778	331		VAC	1.7e-235	264/268	98	(Goebel *et al.*, 1990)
	331		CPX D6L	7.7e-235	264/268	98	(Safronov *et al.*, 1996)
D5L	330		VAR-BSH (I: D3L)	3.6e-233	169/171	97	(Shchelkunov *et al.*, 1995)
	316		VAR-I D11L (BSH:D14L)	1.7e-94	34/68	44	(Shchelkunov *et al.*, 1995)
	316		VAC C4L	1.8e-92	30/68	54	(Goebel *et al.*, 1990)
	315		CPX D16L	2.3e-92	31/68	45	(Safronov *et al.*, 1996)
	82		Ectromelia 42K protein	1.2e-50	78/82	95	(Senkevich *et al.*, 1993a)
	418		FPV BamH1 ORF1	3.0e-11	13/41	31	(Tomley *et al.*, 1988)
007R 12263	91	10.6	28k virulence factor (f)				(Senkevich *et al.*, 1993a)
12538	242		CPX D7R	1.5e-51	42/47	89	(Safronov *et al.*, 1996)
	184		VAC-WR 21.7k protein	5.3e-51	41/47	87	(Kotwal and Moss, 1988a)
D4R	242		VAR-I (BSH:D6R)	3.7e-50	41/47	87	(Shchelkunov *et al.*, 1995)
	241		Ectromelia 28k secreted virulence factor	3.7e-50	41/47	87	(Senkevich *et al.*, 1993a)
008L 13414	120	13.7	13.7k protein				(Shchelkunov *et al.*, 1995)
D7L 13052	126		VAR-BSH (I:D5L)	1.9e-83	57/64	89	(Senkevich *et al.*, 1993a)
	138		Ectromelia 16k protein	7.8e-81	58/60	96	(Safronov *et al.*, 1996)
	124		CPX D8L	3.2e-67	49/60	81	(Kotwal and Moss, 1988a)
	68		7.8k protein (VAC-WR)	1.3e-34	53/64	82	
009L 13745	90	10.7	77k CPX hr protein (f1)				(Spehner *et al.*, 1988)
13473	669		CPX host range gene	2.7e-46	43/52	82	(Safronov *et al.*, 1996)
	634		VAC C9L	1.7e-05	9/33	27	(Goebel *et al.*, 1990)
010L 14186	142	16.1	77k CPX hr protein (f2)				(Spehner *et al.*, 1988)
13758	669		CPX host range gene	2.2e-91	133/142	93	(Safronov *et al.*, 1996)
	634		VAC C9L	9.2e-21	26/63	41	(Goebel *et al.*, 1990)
D6L	452		VAR-I (BSH: D8L)	4.5e-13	27/29	93	(Shchelkunov *et al.*, 1995)
	150		VAC C18L/B24R	1.3e-11	19/52	36	(Goebel *et al.*, 1990)
	439		AT ankyrin repeat protein	9.5e-07	23/59	38	(Zhang *et al.*, 1992)
	558		VAR-I B6R (BSH:B5R)	4.0e-05	28/113	24	(Shchelkunov *et al.*, 1995)
			30 matches with ankyrin repeat containing proteins	2.7e-05 to 0.016			
011L 14682	135	15.8	77k CPX hr protein (f3)				(Spehner *et al.*, 1988)
14275	669		CPX host range gene	7.6e-80	54/64	84	(Safronov *et al.*, 1996)
D6L	452		VAR-I (BSH: D8L)	9.2e-78	52/64	81	(Shchelkunov *et al.*, 1995)
012L 15183	90	10.3	77k CPX hr protein (f4)				(Spehner *et al.*, 1988)

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GENOMIC SEQUENCE OF THE MVA STRAIN

ORF[a]	START STOP	AA[b]	kDa[c]	name / (putative) function / homologies[e]	BLAST[d] expect	BLAST[e] AA id	HSS[f] (%)	references
left terminal region:								
D6L	14911	452		VAR-I (BSH: D8L)	2.2e-52	80/85	94	(Shchelkunov *et al.*, 1995)
		669		CPX host range gene	8.1e-51	77/85	90	(Spehner *et al.*, 1988)
		153		VAR-I D7L (BSH: D10L)	2.9e-17	19/45	42	(Shchelkunov *et al.*, 1995)
		634		VAC C9L	1.3e-13	19/45	42	(Goebel *et al.*, 1990)
		1161		C. botulinum NTNH protein	0.00019	6/12	50	(Hutson *et al.*, 1996)
		202		Capripox	0.00058	15/58	25	(Cao *et al.*, 1995)
		895		UDP glucose dehydrogenase	0.00051	6/19	31	(Bult *et al.*, 1996)
		516		orf virus ank-like	0.0064	16/49	32	(Sullivan *et al.*, 1995b)
		673		rabbit fibroma 77.2k protein	0.0072	12/30	40	(Massung *et al.*, 1992)
013L	15420	71	8.5	77k CPX hr protein (f5)				
	15205	669		CPX host range gene	5.2e-44	68/69	98	(Spehner *et al.*, 1988)
D6L		452		VAR (BSH: D8L)	7.9e-42	64/67	95	(Safronov *et al.*, 1996)
		673		rabbit fibroma 77.2k protein	0.0052	8/26	30	(Shchelkunov *et al.*, 1995)
		386		VAC C17L/B23R	0.018	14/33	42	(Massung *et al.*, 1992)
		202		Capripox	0.023	10/19	52	(Goebel *et al.*, 1990)
		574		VAC B18R (WR: B17R)	0.71	12/28	42	(Sullivan *et al.*, 1995b)
		574		VAR B19R (BSH:B16R)	0.71	12/28	42	(Goebel *et al.*, 1990)
								(Shchelkunov *et al.*, 1995)
014L	16205	109	13.1	75k ank-like gene (f1)				
C9L	15876	634		VAC	3.9e-73	109/109	100	(Kotwal and Moss, 1988a)
		614		CPX D11L	1.6e-70	105/108	97	(Goebel *et al.*, 1990)
D9L		91		VAR (I: D6.5L)	1.2e-52	78/91	85	(Safronov *et al.*, 1996)
		437		CPX D1L	3.7e-19	28/67	41	(Shchelkunov *et al.*, 1995)
		673		rabbit fibroma 77.2K protein	0.021	5/16	31	(Safronov *et al.*, 1996)
015L	16786	96	11.2	75k ank-like gene (f2)				(Massung *et al.*, 1992)
C9L	16496	634		VAC	4.0e-53	80/80	100	(Kotwal and Moss, 1988a)
		614		CPX D11L	3.9e-25	48/80	60	(Goebel *et al.*, 1990)
		437		CPX D1L	9.6e-12	14/36	38	(Safronov *et al.*, 1996)
		172		VAR-Garcia 1966 B11L	0.0001	17/17	100	(Safronov *et al.*, 1996)
		141		integrase (simian foamy v.)	0.033	10/24	41	(Massung *et al.*, 1996)
		669		CPX host range gene	0.043	9/17	52	(Schweizer and Neumann, 1995)
016L	17759	297	35.0	75k ank-like gene (f3)				(Spehner *et al.*, 1988)
C9L	16866	634		VAC	3.4e-208	291/294	98	(Kotwal and Moss, 1988a)
		614		CPX D11L	1.4e-130	90/126	71	(Goebel *et al.*, 1990)
D7L		153		VAR-I (BSH:D10L)	8.4e-68	84/109	77	(Safronov *et al.*, 1996)
		669		CPX host range gene	4.5e-17	24/61	39	(Shchelkunov *et al.*, 1995)
		452		CPX D9L	2,2e-16	23/61	37	(Spehner *et al.*, 1988)
D8L		668		VAR-BSH (I:D6L)	3.3e-16	21/61	34	(Safronov *et al.*, 1996)
		386		VAC C17L/B23R	2.9e-08	11/24	45	(Shchelkunov *et al.*, 1995)
		833		CPX D3L	0.0085	13/58	22	(Goebel *et al.*, 1990)
		574		VAC B18R (WR:B17R)	0.012	13/40	32	(Safronov *et al.*, 1996)
		202		Capripox virus	0.084	11/29	37	(Goebel *et al.*, 1990)
		574		VAR-I B19R (BSH:B16R)	0.090	13/40	32	(Sullivan *et al.*, 1995b)
								(Shchelkunov *et al.*, 1995)
017L	18335	177	20.8	20.8k protein				
C8L	17802	184		VAC	1.2e-125	125/129	96	(Kotwal and Moss, 1988a)
		182		CPX D12L	5.0e-118	119/126	94	(Goebel *et al.*, 1990)
		182		VAC B7R	8.3e-06	16/67	23	(Safronov *et al.*, 1996)
		795		VAC H4L (RAP94)	0.60	12/45	26	(Goebel *et al.*, 1990)
								(Goebel *et al.*, 1990)
018L	18859	150	18.0	host range protein				
C7L	18407	150		VAC	1.6e-106	150/150	100	(Perkus *et al.*, 1991)
D11L		150		VAR-BSH (I:D8L)	4.2e-106	149/150	99	(Kotwal and Moss, 1988a)
		185		Swinepox virus ORF SwF8a	3.4e-35	31/82	37	(Shchelkunov *et al.*, 1995)
		197		Capripox virus ORF CF8a	1.4e-31	29/87	33	(Schnitzlein and Tripathy, 1991)
		170		CPX D4L	3.5e-17	19/60	31	(Gershon and Black, 1989a)
		158		Myxoma virus ORF MF8	5.6e-13	16/43	37	(Safronov *et al.*, 1996)
		128		VAR-BSH D3L (I:D1.5L)	5.4e-06	18/60	30	(Jackson and Bults, 1992)
								(Shchelkunov *et al.*, 1995)
019L	19541	157	18.2	18.2k protein				
C6L	19068	151		VAC	7.6e-104	151/151	100	(Kotwal and Moss, 1988a)
D9L		156		VAR (BSH: D12L)	1.6e-99	145/150	96	(Goebel *et al.*, 1990)
		156		CPX D14L	1.3e-96	141/150	94	(Shchelkunov *et al.*, 1995)
		159		Capripox virus ORF T3a	4.4e-07	24/76	31	(Safronov *et al.*, 1996)
		151		Rabbit fibroma virus T3Aa	0.0047	16/46	34	(Gershon and Black, 1989a)
		181		VAC C16L/B22R	0.2	12/46	26	(Upton *et al.*, 1987)
		149		VAR C4R	0.29	8/13	61	(Goebel *et al.*, 1990)
		149		VAC-WR K7R	0.40	8/13	61	(Shchelkunov *et al.*, 1995)
								(Kotwal and Moss, 1988a)
020L	20025	113	13.2	14k virulence factor,				
	19684			secreted protein (f)				(Kotwal and Moss, 1988a)
N1L		117		VAC				(Kotwal and Moss, 1988b)
		117		CPX P1L	2.6e-60	92/102	90	(Goebel *et al.*, 1990)
P1L		117		VAR-BSH, virokine	7.3e-58	85/102	83	(Shchelkunov *et al.*, 1995)
		107		Rabbit fibroma virus	6.6e-56	88/102	86	(Safronov *et al.*, 1996)
					0.015	10/17	58	(Massung *et al.*, 1992)
021L	20656	170	20.3	alpha-amanitin sensitive				
	20144			protein				(Tamin *et al.*, 1991)
		175		CPX P2L				(Kotwal and Moss, 1988a)
N2L		175		VAC	3.0e-118	138/142	97	(Safronov *et al.*, 1996)
P2L		177		VAR	6.1e-118	137/142	96	(Goebel *et al.*, 1990)
					9.7e-115	135/142	95	(Shchelkunov *et al.*, 1995)
022L	20981	98	11.0	33k host range gene (f)				
K1L	20685	284		VAC				(Gillard *et al.*, 1986)
		284		CPX M1L	1.8e-56	86/88	97	(Altenburger *et al.*, 1989)
C1L		66		VAR	2.3e-56	86/88	97	(Safronov *et al.*, 1996)
		65		human NOTCH 2	2.0e-39	63/66	95	(Shchelkunov *et al.*, 1995)
					0.00036	17/41	41	(Kotsanis *et al.*, 1996)

ORF[a]	START STOP	AA[b]	kDa[c]	name / (putative) function / homologies[g]	BLAST[d] expect	BLAST[e] AA id	HSS[f] (%)	references
left terminal		region:						
023L	22296 21187	369	42.3	serpin SPI-3, cell-cell fusion mutation				(Boursnell *et al.*, 1988) (Altenburger *et al.*, 1989)
K2L		369		VAC	1.2e-258	365/369	98	(Goebel *et al.*, 1990)]
C2L		373		CPX M2L	1.2e-256	331/337		(Safronov *et al.*, 1996)
		373		VAR-BSH	9.9e-249	321/337	95	(Shchelkunov *et al.*, 1995)
		373		Ectromelia virus H14-B	6.5e-244	312/337		U67964
		386		HS plasminogen activator inhibitor 1	1.1e-35	30/68	44	(Loskutoff *et al.*, 1987)
		58		CPX SPI 3 protein	8.2e-33	57/58	98	gi:1168082
		369		Myxoma virus MAP1 gene	7.3e-32	33/131	25	(Upton *et al.*, 1990a)
		397		mouse protease nexin	1.5e-29	31/67	46	(Vassalli *et al.*, 1993)
		397		humane glia derived neurite-promoting factor	8.7e-27	30/65	46	A03911
		320		Swinepox SPI like protein	3.6e-21	20/70	28	(Massung *et al.*, 1993)
		417		a-1 *antitrypsin, human*	2.2e-20	26/66	39	(Ciliberto *et al.*, 1985)
		383		Corticosteroid-binding protein (rabbit)	9.0e-20			(Seralini *et al.*, 1989)
		390		squamous cell carcinoma antigen	1.9e-17			(Schneider *et al.*, 1995)
024L	22612 22346	88	10.5	IFN resistance, eIF-2a homolog				(Beattie *et al.*, 1991) (Davies *et al.*, 1992)
		88		CPX M3L	2.6e-61	88/88	100	(Safronov *et al.*, 1996)
K3L		88		VAC	1.4e-60	87/88	98	(Goebel *et al.*, 1990)
C3L		88		VAR-I	1.0e-52	73/88	82	(Shchelkunov *et al.*, 1995)
		86		SPV C8 protein	4.1e-22	20/44	45	(Massung *et al.*, 1993)
				translation initiation factor 2 family	1.2e-08/ 0.45			
025L	23938 22664	424	48.9	phospholipase D-like protein				(Cao *et al.*, 1997)
K4L		424		VAC	1.5e-306	423/424	99	(Goebel *et al.*, 1990)
		424		CPX M4L	2.1e-303	416/424	98	(Safronov *et al.*, 1996)
		437		human HU-K4	2.8e-135	53/95	55	U60644
		372		D. discoideum	2.5e-91	28/47	59	(Giorda *et al.*, 1989)
		516		C. elegans	6.6e-89	31/61	50	gi: 2435624
		2327		C. elegans	2.8e-52	36/60	60	gi: 2291241
		635		C. elegans	1.1e-24	19/53	35	(Wilson *et al.*, 1994)
		377		FPV major envelope protein	2.9e-23	19/61	31	(Calvert *et al.*, 1992)
		371		Myxoma virus env protein	3.6e-22	18/51	35	U43549
		378		Orf virus *env protein* B2L	1.2e-21	21/71	29	(Sullivan *et al.*, 1994)
MC021L		388		MCV subtype 1 env protein	3.2e-21	20/63	31	(Senkevich *et al.*, 1997)
C17L		372		VAR-BSH	4.6e-19	15/52	28	(Shchelkunov *et al.*, 1995)
		372		VAC F13L	4.9e-17	15/52	28	(Goebel *et al.*, 1990)
026L	24478 23966	170	19.1	lysophospholipase-like protein (f1)				(Upton & Buller, unpub.)
		276		CPX M5L	2.6e-110	161/170	94	(Safronov *et al.*, 1996)
		277		Ectromelia virus H14-E	2.7e-109	160/170	94	X94355 U67964
K5L		136		VAC	5.5e-69	107/108	99	(Goebel *et al.*, 1990)
		134		VAC-WR	8.3e-63	98/101	97	(Boursnell *et al.*, 1988)
		313		HS lysophospholipase	3.3e-35	35/105	33	U67963
		323		homolog	1.2e-13	30/94	31	Z97050
		324		poss. oxidoreductase M. tuberculosum	3.1e-5	13/58	22	U95973
		313		Lysophospholipase isolog A. thaliana	0.047	13/30	43	U32747
				H. influenza probable lysophospholipase L2				
027L	24694 24500	64	7.0	lysophospholipase-like protein (f2)				(Upton & Buller, unpub.)
K6L		81		VAC	5.3e-42	63/63	100	(Boursnell *et al.*, 1988)
		276		CPX M5L	2.4e-36	57/58	98	(Safronov *et al.*, 1996)
		277		Ectromelia virus H14-E	2.4e-36	57/58	98	U67964
		313		HS lyophospholipase homolog	9.1e-23	34/53	64	U67963
		323		hyp. oxidoreductase M. *tuberculosis*	9.9e-14	22/54	40	Z97050
		530		dihydrotestosterone/androstanediol UDP-glucuronosyl-transferase	7.0e-05	6/17	35	A48633
central	conserved	region:						
028R	24864	149	17.5	17.5k protein				(Goebel *et al.*, 1990)
K7R	25313	149		VAC	6.1e-105	149/149	100	(Goebel *et al.*, 1990)
		161		CPX M6R	1.6e-101	144/149	96	(Safronov *et al.*, 1996)
C4R		149		VAR	4.9e-101	143/149	100	(Shchelkunov *et al.*, 1995)
		236		Swinepox (sc76)	0.00017	19/49	95	(Massung *et al.*, 1993)
029L	26046	222	25.9	25.9k protein				(Roseman and Slabaugh, 1990)
F1L	25378	226		VAC	2.7e-158	208/211	98	(Goebel *et al.*, 1990)
		238		CPX G1L	7.0e-148	166/189	87	(Safronov *et al.*, 1996)
C5L		251		VAR-1	6.6e-147	184/200	92	(Shchelkunov *et al.*, 1995)
030L	26501 26058	147	16.2	dUTPase				(Roseman and Slabaugh, 1990) (Roseman *et al.*, 1996)
F2L		147		VAC	2.9e-102	147/147	100	(Goebel *et al.*, 1990)
		147		CPX G2L	8.2e-100	144/147	97	(Safronov *et al.*, 1996)
C6L		147		VAR	1.1e-97	142/147	96	(Shchelkunov *et al.*, 1995)
		164		human dUTPase	4.1e-61	49/69	71	(Ladner *et al.*, 1996)

GENOMIC SEQUENCE OF THE MVA STRAIN

ORF[a]	START STOP	AA[b]	kDa[c]	name / (putative) function / homologies[f]	BLAST[d] expect	BLAST[e] AA id	HSS[f] (%)	references
left terminal region:								
		142		Swinepox virus	8.0e-56	43/70	61	(Massung *et al.*, 1993)
		159		orf virus	1.5e-49	45/69	65	(Mercer *et al.*, 1989)
		178		avian adenovirus	6.6e-49	40/70	57	(Akopian *et al.*, 1992)
		1124		FIV pol polyprotein	1.5e-26	49/117	41	(Talbott *et al.*, 1989)
				dUTPase pyrophosphatase family	>4.2e-06			
031L	27955 26525	476	55.3	**kelch-like protein**				(Senkevich *et al.*, 1993b)
F3L		480		VAC	0.0	292/294	99	(Roseman and Slabaugh, 1990)
		485		CPX G3L	0.0	287/293	97	(Goebel *et al.*, 1990)
C7L		179		VAR-1	1.9e-124	166/179	92	(Safronov *et al.*, 1996)
		500		Swinepox virus protein C13	4.4e-46	39/133	29	(Shchelkunov *et al.*, 1995)
		564		VAC A55R	2.8e-21	17/51	33	(Massung *et al.*, 1993)
		689		kelch protein D.melanogaster	5.3e-18	21/65	32	(Goebel *et al.*, 1990)
		512		CPX D18L	1.4e-16	15/33	45	(Xue and Cooley, 1993)
		512		VAC C2L	1.6e-16	15/33	45	(Safronov *et al.*, 1996)
		625		T27E9.4 C. elegans	3.7e-14	15/59	25	(Goebel *et al.*, 1990)
		624		human KIAA0132 protein	1.9e-13	13/60	21	Z82059
		817		R09A8.3 (C. elegans)	1.1e-12	17/45	37	D50922 o.k
		611		C47D12.7 (C. elegans)	2.4e-12	22/91	24	(Wilson *et al.*, 1994)
		530		Swinepox virus	3.0e-09	14/58	24	(Wilson *et al.*, 1994)
		589		MM[m] actin binding protein	1.9e-09	18/88	20	(Massung *et al.*, 1993)
		521		CPX C3L	1.2e-08	15/37	40	U65079
		509		Myxoma virus MT-9	2.5e-08	17/58	29	(Safronov *et al.*, 1996)
		202		Murine IAP-promoted placenta (MIPP) expressed protein	4.3e-08	17/56	30	(Upton *et al.*, 1990a) (Chang-Yeh *et al.*, 1991)
		326			3.9e-06	22/80	27	Z99708
		559		A. thaliana hyp. protein	9.0e-6	12/31	38	(Senkevich *et al.*, 1993b)
		916		Ectromelia virus p65	0.00016	13/42	30	(Way *et al.*, 1995)
		172		ß-scruin (L. polyphemus) VAR-I J8R (BSH: J6R)	0.018	15/36	41	(Shchelkunov *et al.*, 1995)
032L	28925 27966	319	37.0	**ribonucleotide reductase (small subunit)**				(Slabaugh *et al.*, 1988) (Roseman and Slabaugh, 1990)
		319		CPX G4L	2.3e-231	317/319	99	(Safronov *et al.*, 1996)
F4L		319		VAC	3.5e-231	317/319	99	(Goebel *et al.*, 1990)
C8L		333		VAR-BSH	4.1e-228	313/319	98	(Shchelkunov *et al.*, 1995)
				ribonucleotide reductase family	>2.2e-10			
033L	29250 28957	97	11.1	**36.5k major membrane protein precursor (f1)**				(Roseman and Slabaugh, 1990)
C9L		348		VAR-BSH	1.9e-36	51/53	96	(Shchelkunov *et al.*, 1995)
		323		CPX G5L	2.4e-19	47/77	61	(Safronov *et al.*, 1996)
F5L		321		VAC	3.3e-19	42/70	60	(Goebel *et al.*, 1990)
		1584		non-receptor tyrosin kinase (Dictyostelium discoideum)	0.00038	15/35	42	(Tan and Spudich, 1990)
034L	29875 29219	218	24.8	**36.5k major membrane protein precursor (f2)**				(Roseman and Slabaugh, 1990)
		323		CPX G5L	8.2e-155	215/217	99	(Safronov *et al.*, 1996)
F5L		321		VAC	6.4e-155	215/217	99	(Goebel *et al.*, 1990)
C9L		348		VAR-BSH	6.8e-141	186/210	88	(Shchelkunov *et al.*, 1995)
035L	30129	74	8.6	**8.6k protein**				(Roseman and Slabaugh, 1990)
F6L	29905	74		VAC	5.5e-47	74/74	100	(Goebel *et al.*, 1990)
C10L		72		VAR	2.3e-38	62/70	88	(Shchelkunov *et al.*, 1995)
036L	30387	80	9.4	**9.4k protein**				(Roseman and Slabaugh, 1990)
C11L	30145	79		VAR	2.9e-44	34/43	79	(Shchelkunov *et al.*, 1995)
F7L		92		VAC	1.9e-43	65/65	100	(Goebel *et al.*, 1990)
037L	30731	65	7.9	**7.9k protein**				(Roseman and Slabaugh, 1990)
F8L	30534	65		VAC	5.1e-43	63/65	96	(Goebel *et al.*, 1990),
C12L		65		VAR-I	3.1e-41	61/65	93	(Shchelkunov *et al.*, 1995)
038L	31429 /	212	23.8	**23.8k protein**				(Roseman and Slabaugh, 1990)
F9L	30791	212		VAC	7.1e-148	212/212	100	(Goebel *et al.*, 1990),
C13L		212		VAR	1.2e-144	207/212	97	(Shchelkunov *et al.*, 1995)
		215		Swinepox virus	8.1e-72	39/93	41	(Massung *et al.*, 1993)
MC016L		213		MCV subtype 1	2.8e-62	71/152	46	(Senkevich *et al.*, 1996)
		225		Orf virus	5.1e-39	27/84	32	(Mercer *et al.*, 1995)
		243		FPV protein FP2	2.8e-17	26/58	44	(Binns *et al.*, 1988)
		243		MCV subtype 1 MC069R	7.7e-12	23/58	39	(Senkevich *et al.*, 1996)
		250		VAC LIR	1.1e-07	20/58	34	(Goebel *et al.*, 1990),
		250		VAR MIR	1.1e-07	20/58	34	(Shchelkunov *et al.*, 1995)
039L	32735 31416	439	52.1	**serine/threonine protein kinase 2**				(Lin and Broyles, 1994) (Wang and Shuman, 1995)
F10L		439		VAC	0.0	429/439	97	(Goebel *et al.*, 1990),
C14L		439		VAR-BSH	0.0	424/439	96	(Shchelkunov *et al.*, 1995)
		440		Swinepox virus	2.2e-233	151/214	70	(Massung *et al.*, 1993)
MC017L		443		MCV subtype 1	2.3e-198	178/282	63	(Senkevich *et al.*, 1996)
		498		orf virus	2.2e-162	198/366	54	(Mercer *et al.*, 1995)
040L	33012	84	9.6	**39.7k protein (f1)**				
C15L	32758	354		VAR	6.6e-27	50/64	78	(Shchelkunov *et al.*, 1995)
F11L		354		VAC	9.1e-27	50/64	78	(Goebel *et al.*, 1990)
041L	33771	100	11.4	**39.7k protein (f2)**				

ORF[a]	START STOP	AA[b]	kDa[c]	name / (putative) function / homologies[e]	BLAST[d] expect	BLAST[e] AA id	HSS[f] (%)	references
left terminal		region:						
F11L	33469	354		VAC	3.8e-62	95/95	100	(Goebel *et al.*, 1990),
C15L		354		VAR	8.8e-58	90/95	94	(Shchelkunov *et al.*, 1995)
042L	35721	635	73.1	**73.1k protein**				
F12L	33814	635		VAC	0.0	629/635	99	(Goebel *et al.*, 1990),
C16L		635		VAR-I	0.0	607/635	95	(Shchelkunov *et al.*, 1995)
		352		Myxoma virus	3.6e-84	28/66	42	U43549
MC019L		663		MCV subtype I	4.0e-60	29/82	35	(Senkevich *et al.*, 1996)
		640		orf virus	4.8e-39	19/61	31	U34774
		630		FPV F12 homolog	2.3e-15	19/67	28	(Ogawa *et al.*, 1993)
043L	36866 35748	372	41.8	**37k major EEV antigen IMCBH sensitive protein palmitylprotein**				(Hirt *et al.*, 1986) (Schmutz *et al.*, 1991) (Grosenbach *et al.*, 1997)
F13L		372		VAC	2.1e-268	369/372	99	(Goebel *et al.*, 1990)
C17L		372		VAR-BSH	8.9e-265	364/372	97	(Shchelkunov *et al.*, 1995)
		371		Myxoma virus	2.5e-115	110/200	55	U43549
		378		orf virus	7.6e-108	83/194	42	(Sullivan *et al.*, 1994)
MC021L		388		MCV subtype I	6.1e-98	44/113	38	(Senkevich *et al.*, 1996)
		377		FPV major env protein	2.8e-88	47/112	41	(Calvert *et al.*, 1992)
		251		pigeonpox virus	1.8e-62	47/112	41	S27933
		424		CPXM4L	2.1e-18	16/52	30	(Safronov *et al.*, 1996)
		424		VAC K4L	1.7e-17	14/35	40	(Goebel *et al.*, 1990)
		372		D. discoideum	1.4e-16	28/84	33	(Giorda *et al.*, 1989)
		437		HU-K4 (homo sapiens)	1.5e-11	25/94	26	U60644
044L	37105	73	8.3	**8.3k protein**				
F14L	36884	73		VAC	2.3e-44	72/73	98	(Goebel *et al.*, 1990)
C18L		73		VAR	2.1e-35	57/73	78	(Shchelkunov *et al.*, 1995)
045L	378533	158	18.6	**18.6k protein**				
F15L	37377	158		VAC	2.3e-112	157/158	99	(Goebel *et al.*, 1990),
C19L		161		VAR	1.4e-107	150/153	98	(Shchelkunov *et al.*, 1995)
MC025L		148		MCV subtype I	3.5e-54	52/113	46	(Senkevich *et al.*, 1996)
		148		Myxoma virus	5.4e-50	48/112	42	U43549
046L	38555	231	26.5	**26.5k protein**				
F16L	37860	231		VAC	3.3e-159	227/231	98	(Goebel *et al.*, 1990),
C20L		231		VAR	5.6e-157	222/231	96	(Shchelkunov *et al.*, 1995)
		209		Myxoma virus	8.3e-48	26/58	44	U43549
MC029L		230		MCV subtype I	6.9e-45	16/61	26	(Senkevich *et al.*, 1996)
047R	38619 38924	101	11.3	**11k DNA binding phosphoprotein**				(Bertholet *et al.*, 1985) (Kao and Bauer, 1987)
F17R		101		VAC	3.0e-69	100/101	99	(Goebel *et al.*, 1990)
C21R		101		VAR	9.7e-67	99/101	98	(Shchelkunov *et al.*, 1995)
		102		MYX	6.6e-26	45/92	98	U43549
MC030R		92		MCV subtype I	1.5e-20	33/53	48	(Senkevich *et al.*, 1997)
		46		orf virus	1.3e-06	16/29	62	(Mercer *et al.*, 1995)
048L	40360 38921	479	55.6	**poly(A) polymerase catalytic subunit**				(Gershon *et al.*, 1991)
E1L		479		VAC	0.0	478/479	99	(Goebel *et al.*, 1990),
E1L		479		VAR-I	0.0	472/479	98	(Shchelkunov *et al.*, 1995)
MC031L		470		MCV subtype I	1.5e-177	114/173	65	(Senkevich *et al.*, 1997)
049L	42570	737	85.9	**85.9k protein**				(Ahn *et al.*, 1990a)
E2L	40357	737		VAC	0.0	735/737	99	(Goebel *et al.*, 1990),
E2L		737		VAR-I	0.0	731/737	99	(Shchelkunov *et al.*, 1995)
MC032L		748		MCV subtype I	8.3e-127	59/198	29	(Senkevich *et al.*, 1997)
050L	43269 42697	190	21.5	**dsRNA dependent PK inhibitor, host range**				(Chang *et al.*, 1992) (Chang *et al.*, 1995b)
E3L		190		VAC	1.4e-129	188/190	98	(Goebel *et al.*, 1990),
E3L		192		VAR-BSH	8.6e-126	111/114	97	(Shchelkunov *et al.*, 1995)
		1175		dsRNA specific ADA (rat)	7.2e-12	22/47	46	(O'Connell *et al.*, 1995)
		1226		dsRNA specific ADA (human)	2.8e-09	21/47	44	(Kim *et al.*, 1994)
		551		human protein kinase p68	3.8e-05	22/42	52	(Meurs *et al.*, 1990)
				INF inducible kinase family	>0.00099			
051L	44103 43324	259	29.8	**RNA polymerase subunit rpo30, VITF-1**				(Ahn *et al.*, 1990a) (Broyles and Pennington, 1990)
E4L		259		VAC	1.6e-182	258/259	99	(Goebel *et al.*, 1990)
E4L		259		VAR-BSH	3.2e-180	255/259	98	(Shchelkunov *et al.*, 1995)
MC034L		444		MCV subtype I	1.2e-84	107/171	62	(Senkevich *et al.*, 1996)
		39		orf virus	6.7e-10	21/39	53	(Mercer *et al.*, 1995)
		243		African swine fever virus TFIIS family	0.00034 <0.0096	17/36	47	(Vydelingum *et al.*, 1993)
052R	44180	331	39.1	**39.1k protein**				(Goebel *et al.*, 1990)
E5R	45175	331		VAC	1.2e-235	329/331	99	(Goebel *et al.*, 1990)
E5R		341		VAR	3.1e-223	312/331	94	(Shchelkunov *et al.*, 1995)
		332		Taterapox	7.1e-225	300/314	95	(Douglas and Dumbell, 1996)
		329		Camelpox	1.4e-221	206/220	93	(Douglas and Dumbell, 1996)
		319		Cowpox	1.5e-202	271/303	89	(Douglas and Dumbell, 1996)
		256		Ectromelia	3.8e-153	218/245	88	(Douglas and Dumbell, 1996)
MC038R		276		MCV subtype I	8.3e-109	94/152	61	(Senkevich *et al.*, 1997)
053R	45312	567	66.7	**66.7k protein**				(Goebel *et al.*, 1990)

GENOMIC SEQUENCE OF THE MVA STRAIN

ORF[a]	START STOP	AA[b]	kDa[c]	name / (putative) function / homologies[e]	BLAST[d] expect	BLAST[e] AA id	HSS[f] (%)	references
left terminal		region:						
E6R		567		VAR	0.0	555/567	97	(Shchelkunov *et al.*, 1995)
MC037R		565		MCV subtype 1	7.2e-247	258/451	57	(Senkevich *et al.*, 1997)
054R	47082	166	19.5	17k myristylprotein				
E7R	47582	166		VAC	9.7e-116	166/166	100	(Martin *et al.*, 1997)
E7R		60		VAR-1 (BSH: E6.5R)	2.7e-36	53/60	88	(Goebel *et al.*, 1990)
								(Shchelkunov *et al.*, 1995)
055R	47695	273	31.9	31.9k protein				
E8R	48516	273		VAC	4.5e-195	272/273	99	(Earl *et al.*, 1986)
E8R		273		VAR	9.9e-192	266/273	99	(Goebel *et al.*, 1990)
MC038R		276		MCV subtype 1	8.3e-109	94/152	97	(Shchelkunov *et al.*, 1993a),
								(Senkevich *et al.*, 1997)
056L	51543	1006	116.9	DNA polymerase				
E9L	48523	1006		VAC	0.0	1005/10	99	(Earl *et al.*, 1986)
E9L		1005		VAR BSH	0.0	06	98	(Goebel *et al.*, 1990),
		1008		Orf virus	0.0	598/608	51	(Shchelkunov *et al.*, 1995)
		988		FPV	0.0	199/388	60	(Mercer *et al.*, 1996)
MC039L		1004		MCV subtype 1	0.0	179/294	58	(Binns *et al.*, 1987)
		964		C. biennis poxvirus	2.6e-77	175/297	34	(Senkevich *et al.*, 1997)
				DNA polymerase family	>6.0e-06	28/82		(Mustafa and Yuen, 1991)
057R	51575	95	10.9	10.9k protein				
E10R	51862	95		VAC	1.2e-65	93/95	97	(Goebel *et al.*, 1990)
E10R		95		VAR	3.1e-64	90/95	100	(Goebel *et al.*, 1990)
MC040R		101		MCV subtype 1	5.2e-44	58/95	94	(Shchelkunov *et al.*, 1993a)
								(Senkevich *et al.*, 1997)
058L	52246	129	14.9	14.9k protein				
E11L	51857	129		VAC	3.3e-89	129/129	100	(Goebel *et al.*, 1990)
E11L		129		VAR	4.2e-87	125/129	96	(Goebel *et al.*, 1990)
MC041L		132		MCV subtype 1	1.8e-30	31/96	32	(Shchelkunov *et al.*, 1995)
								(Senkevich *et al.*, 1997)
059L	52691	152	17.6	77.6k protein (f1)				
O1L	52233	666		VAC	6.9e-101	151/152	99	(Goebel *et al.*, 1990)
Q1L		666		VAR-BSH	3.4e-92	137/152	90	(Goebel *et al.*, 1990),
MC042L		783		MCV subtype 1	1.5e-22	39/105	37	(Shchelkunov *et al.*, 1995)
				leu zipper, bipartite nuclear targeting sequence				(Senkevich *et al.*, 1997)
								(Goebel *et al.*, 1990)
060L	54189	405	47.4	77.6k protein (f2)				
O1L	52972	666		VAC	5.8e-277	399/400	99	(Goebel *et al.*, 1990)
Q1L		666		VAR-1	1.7e-269	383/400	95	(Goebel *et al.*, 1990)
MC042L		783		MCV subtype 1	2.7e-51	38/104	36	(Shchelkunov *et al.*, 1995)
								(Senkevich *et al.*, 1997)
061L	54555	108	12.4	glutaredoxin 1				
	54229							(Ahn and Moss, 1992a)
O2L		108		VAC	2.0e-74	108/108	100	(Johnson *et al.*, 1991)
Q2L		108		VAR	4.9e-72	104/108	96	(Goebel *et al.*, 1990)
		106		human glutaredoxin	3.2e-31	49/106	46	(Shchelkunov *et al.*, 1995)
				glutaredoxin family	>9.0e-05			(Fernando *et al.*, 1994)
062L	55639	312	35.9	35.9k protein				
I1L	54701	312		VAC	4.7e-208	310/312	99	(Schmitt and Stunnenberg, 1988)
K1L		312		VAR-BSH	4.8e-205	305/312	97	(Goebel *et al.*, 1990)
MC044L		310		MCV subtype 1	3.8e-110	163/307	53	(Shchelkunov *et al.*, 1995)
		1451		transcription initiation protein (S. cerevisiae)	0.029	10/28	35	(Senkevich *et al.*, 1996) (Hansen *et al.*, 1996)
063L	55867	73	8.5	8.5k protein				
I2L	55646	73		VAC	5.5e-50	73/73	100	(Schmitt and Stunnenberg, 1988)
K2L		73		VAR	5.5e-50	73/73	100	(Goebel *et al.*, 1990)
MC045L		72		MCV subtype 1	3.5e-18	20/33	60	(Shchelkunov *et al.*, 1995)
		887		hypothetical yeast protein	8.1e-05	9/24	37	(Senkevich *et al.*, 1996)
								S48422
064L	56677	269	30.0	DNA binding phospho-protein (F4L interacting)				(Schmitt and Stunnenberg, 1988)
	55868							(Davis and Mathews, 1993)
I3L		269		VAC	2.1e-173	267/269	99	(Goebel *et al.*, 1990)
K3L		269		VAR	2.5e-172	265/269	98	(Shchelkunov *et al.*, 1995)
MC046L		288		MCV subtype 1	9.6e-66	61/149	40	(Senkevich *et al.*, 1996)
		209		FPV I3 protein	8.4e-35	23/66	34	A48563
065L	59075	771	87.8	ribonucleotide reductase (large subunit)				(Schmitt and Stunnenberg, 1988)
	56760							(Tengelsen *et al.*, 1988)
I4L		771		VAC	0.0	771/771	100	(Goebel *et al.*, 1990)
K4L		771		VAR	0.0	761/771	98	(Shchelkunov *et al.*, 1995)
				ribonucleotide red. family	>1.8e-05			
066L	59342	79	8.8	8.8k protein				(Schmitt and Stunnenberg, 1988)
I5L	59103	79		VAC	6.3e-49	79/79	100	(Goebel *et al.*, 1990)
K5L		79		VAR	1.2e-47	76/79	96	(Shchelkunov *et al.*, 1995)
MC047L		82		MCV subtype 1	2.6e-17	27/73	36	(Senkevich *et al.*, 1996)
		81		FPV 9.1k protein	1.4e-12	13/38	34	(Binns *et al.*, 1988)
		321		formate dep. nitrit reductase protein (H. influenzae)	0.00022	7/18	38	(Fleischmann *et al.*, 1995)
		496		permease (b. subtilis)	0.00031	12/43	27	gi:2415386
067L	60509	382	43.5	43.5k protein				(Schmitt and Stunnenberg, 1988)
I6L	59361	382		VAC	8.6e-268	382/382	100	(Goebel *et al.*, 1990)
K6L		382		VAR	3.1e-267	380/382	99	(Shchelkunov *et al.*, 1995)
MC048L		406		MCV subtype 1	2.1e-99	44/119	36	(Senkevich *et al.*, 1996)

ORF[a]	START STOP	AA[b]	kDa[c]	name / (putative) function / homologies[f]	BLAST[d] expect	BLAST[e] AA id	HSS[f] (%)	references
left terminal region:								
		390		FPV I6 protein mitochondrial energy transfer proteins signature	1.4e-86	50/136	36	E48563, P12925 (Goebel *et al.*, 1990)
068L	61773 60502	423	49.0	core protein, topoisomerase II				(Schmitt and Stunnenberg, 1988) (Kane and Shuman, 1993)
I7L		423		VAC	0.0	420/423	99	(Goebel *et al.*, 1990)
K7L		423		VAR	1.5e-306	419/423	99	(Shchelkunov *et al.*, 1995)
MC049L		515		MCV subtype 1	1.9e-199	126/207	60	(Senkevich *et al.*, 1996)
		421		FPV I7 protein	8.1e-180	185/340	54	F48563
		464		Amsacta moorei poxvirus	3.2e-14	14/47	29	(Hall and Moyer, 1991)
069R	61776 63809	676	77.6	NPH-II, NTPase, RNA helicase				(Shuman, 1992), (Koonin and Senkevich, 1992)
I8R		676		VAC	0.0	674/676	99	(Goebel *et al.*, 1990)
K8R		676		VAR	0.0	665/676	98	(Shchelkunov *et al.*, 1995)
MC050R		684		MCV subtype 1	7.6e-227	144/272	52	(Senkevich *et al.*, 1997)
		682		FPV virus I8FPV	4.2e-206	98/178	55	(Binns *et al.*, 1988)
				61 matches mainly to RNA helicase family	<0.38			
070L	65588	591	68.0	68k protein				(Schmitt and Stunnenberg, 1988)
G1L	63813	591		VAC	0.0	590/591	99	(Goebel *et al.*, 1990)
H1L		591		VAR-1	0.0	582/591	98	(Shchelkunov *et al.*, 1995)
MC056L		593		MCV subtype 1	1.2e-217	183/361	50	(Senkevich *et al.*, 1997)
		341		FPV	9.4e-75	45/101	44	H48563
071L	65920 65585	111	12.8	12.8k protein				(Schmitt and Stunnenberg, 1988) (Meis and Condit, 1991)
G3L		111		VAC	7.6e-74	111/111	100	(Goebel *et al.*, 1990)
H3L		111		VAR	2.4e-71	108/111	97	(Shchelkunov *et al.*, 1995)
MC057L		108		MCV subtype 1	0.00012	15/45	33	(Senkevich *et al.*, 1997)
072R	65914	220	25.8	IBT-dependent protein				(Meis and Condit, 1991)
G2R	66576	220		VAC	1.9e-155	220/220	100	(Goebel *et al.*, 1990)
H2R		220		VAR	1.1e-151	214/220	97	(Shchelkunov *et al.*, 1995)
MC058R		246		MCV subtype 1	2.7e-36	42/135	31	(Senkevich *et al.*, 1997)
073L	66920 66546	124	14.0	glutaredoxin 2 membrane protein				(Gvakharia *et al.*, 1996) (Jensen *et al.*, 1996)
H4L		124		VAR	4.0e-83	123/124	99	(Shchelkunov *et al.*, 1995)
G4L		124		VAC	7.5e-83	123/124	99	(Goebel *et al.*, 1990)
MC059L		126		MCV subtype 1	1.1e-21	21/51	41	(Senkevich *et al.*, 1997)
074R	66923	434	49.9	49.8k protein				(Goebel *et al.*, 1990)
G5R	68227	434		VAC	1.6e-305	432/434	99	(Goebel *et al.*, 1990)
H5R		434		VAR	1.9e-299	423/434	97	(Shchelkunov *et al.*, 1995)
MC60R		437		MCV subtype 1	1.0e-55	56/119	47	(Senkevich *et al.*, 1997)
		1300		HS CG1 protein	0.015	22/82	26	(Print *et al.*, 1994)
075R	68235 68426	63	7.3	RNA polymerase subunit rpo7				(Amegadzie *et al.*, 1992), (Meis and Condit, 1991)
G5.5R		63		VAC	1.1e-40	63/63	100	(Goebel *et al.*, 1990)
H5.5R		63		VAR	1.1e-39	61/63	96	(Shchelkunov *et al.*, 1995)
MC061R		63		MCV subtype 1	9.3e-27	41/63	65	(Senkevich *et al.*, 1997)
				35 matches mainly to RNA polymerases	<0.54			
076R	68428	165	19.0	18.9k protein				(Goebel *et al.*, 1990)
G6R	68925	165		VAC	3.8e-116	162/165	98	(Goebel *et al.*, 1990)
H6R		165		VAR	1.5e-116	164/165	99	(Shchelkunov *et al.*, 1995)
MC062R		195		MCV subtype 1	3.0e-32	27/57	47	(Senkevich *et al.*, 1997)
077L	70005	371	42.0	42.0k protein				(Schmitt and Stunnenberg, 1988)
G7L	68890	371		VAC	5.2e-255	370/371	99	(Goebel *et al.*, 1990)
H7L		371		VAR	7.1e-255	369/371	99	(Shchelkunov *et al.*, 1995)
MC065L		402		MCV subtype 1	2.0e-109	69/145	47	(Senkevich *et al.*, 1997)
078R	70036 70818	260	29.9	VLTF-1, late transcription factor				(Keck *et al.*, 1990) (Wright *et al.*, 1991)
G8R		260		VAC	8.6-184	259/260	99	(Goebel *et al.*, 1990)
H8R		260		VAR-1	3.1e-183	258/260	99	(Shchelkunov *et al.*, 1995)
MC067R		260		MCV subtype 1	8.5e-136	185/260	71	(Senkevich *et al.*, 1997)
		260		FPV virus FPO	3.3e-129	175/250	67	(Binns *et al.*, 1988)
079R	70838	340	38.9	37k myristylprotein				(Martin *et al.*, 1997)
G9R	71860	340		VAC	3.7e-237	317/319	99	(Goebel *et al.*, 1990)
H9R		340		VAR	9.1e-236	315/319	98	(Shchelkunov *et al.*, 1995)
MC068R		342		MCV subtype 1	4.8e-79	59/127	46	(Senkevich *et al.*, 1997)
		336		FPV virus FP1	3.9e-65	59/124	47	(Binns *et al.*, 1988)
080R	71861 72613	250	27.3	25k myristylprotein IMV virion protein				(Franke *et al.*, 1990) (Martin *et al.*, 1997)
L1R		250		VAC	1.8e-175	250/250	100	(Goebel *et al.*, 1990)
M1R		250		VAR	6.4e-170	249/250	99	(Shchelkunov *et al.*, 1995)
MC069R		243		MCV subtype 1	6.5e-103	145/243	59	(Senkevich *et al.*, 1997)
		243		FPV virus FP2	6.2e-95	128/243	52	(Binns *et al.*, 1988)
		212		VAC F9L	1.6e-0.7	20/58	34	(Goebel *et al.*, 1990)
		212		VAR C13L	3.1e-0.7	20/58	34	(Shchelkunov *et al.*, 1995)

ORF[a]	START STOP	AA[b]	kDa[c]	name / (putative) function / homologies[f]	BLAST[d] expect	BLAST[e] AA id	HSS[f] (%)	references
left terminal region:								
		213		MCV subtype I MC016L	1.6e-0.7	13/57	22	(Senkevich *et al.*, 1997)
		215		swinepox	3.3e-0.5	15/51	29	(Massung *et al.*, 1993)
081R	72645	87	10.3	10.3k protein				
L2R	72908	87		VAC				(Plucienniczak *et al.*, 1985)
M2R		87		VAR	3.9e-57	87/87	100	(Goebel *et al.*, 1990)
MC070R		93		MCV subtype I	4.0e-56	85/87	97	(Shchelkunov *et al.*, 1995)
		504		Na^+ dependent phosphate transporter C. elegans	0.064	18/80	22	(Senkevich *et al.*, 1997)
					6.9e-05	10/39	25	(Wilson *et al.*, 1994)
		233		ATPase subunit T. cruzi	0.013	16/44	36	U38184
		2336		Ca^{2+} channel rat	5.2e+0.2	6/25	24	(Dubel *et al.*, 1992)
		2238		Ca^{2+} channel mouse	7.1e+0.2	6/25	24	(Coppola *et al.*, 1994)
		1559		ABC transporter yeast	0.40	12/40	30	X97560
082L	73950	350	40.6	40.6k protein				
L3L	72898	350		VAC				(Plucienniczak *et al.*, 1985)
M3L		349		VAR	2.2e-251	346/350	98	(Goebel *et al.*, 1990)
MC072L		310		MCV subtype I	1.5e-241	296/306	96	(Shchelkunov *et al.*, 1995)
		301		FPV F4 protein	1.5e-88	64/136	47	(Senkevich *et al.*, 1997)
					1.1e-80	58/134	43	(Binns *et al.*, 1988)
083R	73975	251	28.5	core protein VP8				
	74730			DNA/RNA binding protein				(Yang and Bauer, 1988)
L4R		251		VAC				(Baylis and Smith, 1997)
M4R		251		VAR	5.6e-170	251/251	100	(Goebel *et al.*, 1990)
MC073R		254		MCV subtype I	3.7-169	250/251	99	(Shchelkunov *et al.*, 1995)
		253		FPV virus FP5	1.7e-76	36/59	61	(Senkevich *et al.*, 1997)
					6.4e-55	29/57	50	(Binns *et al.*, 1988)
084R	74740	128	15.1	15.1k protein				
L5R	75126	128		VAC 14.0k protein	2.9e-89	127/128	99	(Goebel *et al.*, 1990)
M5R		128		VAR	2.0-87	125/128	97	(Shchelkunov *et al.*, 1995)
-		129		FPV FP6	8.1e-16	19/45	42	(Drillien *et al.*, 1987)
MC074R		146		MCV subtype I	0.073	10/18	55	(Senkevich *et al.*, 1997)
		152		melatonin receptor D. rerio	0.44	15/66	222	(Reppert *et al.*, 1995)
085R	75083	153	17.9	dimeric virion protein				
J1R	75544	153		VAC				(Holzer & Falkner, unpubl.)
L1R		159		VAR-I	6.0e-103	152/153	99	(Goebel *et al.*, 1990)
		147		capripox CF7	1.4e-101	149/153	97	(Shchelkunov *et al.*, 1995)
		148		myxoma MF7	6.5e-54	53/90	58	(Gershon and Black, 1989b)
		183		MCV subtype I	4.8e-51	54/93	58	(Jackson and Bults, 1992)
MC075R		148		FPV FP7	1.9e-47	47/93	50	(Senkevich *et al.*, 1997)
					1.3e-35	37/84	44	(Drillien *et al.*, 1987)
086R	75560	177	20.0	thymidine kinase				
	76093							(Hruby and Ball, 1982)
J2R		177		VAC				(Weir and Moss, 1983)
L2R		177		VAR	5.7e-125	175/177	98	(Goebel *et al.*, 1990)
				38 matches mainly to thymidine kinase family	2.7e-122	170/177	96	(Shchelkunov *et al.*, 1995)
					<0.18			
087R	76159	333	38.9	poly(A) polymerase su, 2'methyl transferase				
	77160							(Gershon *et al.*, 1991)
J3R		333		VAC				(Gershon and Moss, 1993)
L3R		333		VAR-BSH	8.7e-136	330/333	99	(Goebel *et al.*, 1990)
		338		myxoma	9.8e-233	326/333	97	(Shchelkunov *et al.*, 1995)
MC076R		343		MCV subtype I	5.7e-288	247/333	74	(Jackson and Bults, 1990)
		308		FPV VP39	1.4e-135	79/144	54	(Senkevich *et al.*, 1997)
					1.7e-96	125/267	46	(Binns *et al.*, 1988)
088R	77075	185	21.3	RNA pol subunit rpo22				
J4R	77632	185		VAC				(Broyles and Moss, 1986)
L4R		185		VAR-BSH	1.2e-125	185/185	100	(Goebel *et al.*, 1990)
		185		myxoma	7.9e-125	182/185	98	(Shchelkunov *et al.*, 1995)
MC077R		187		MCV subtype I	1.5e-86	124/185	67	(Jackson and Bults, 1990)
		186		FPV	1.9e-76	73/132	55	(Senkevich *et al.*, 1997)
					2.1e-73	72/135	53	(Binns *et al.*, 1988)
089L	78101	133	15.2	15.2k protein				
J5L	77700	133		VAC				(Plucienniczak *et al.*, 1985)
L5L		133		VAR-I	2.4e-95	133/133	100	(Goebel *et al.*, 1990)
MC078L		134		MCV subtype I	2.4e-94	131/133	98	(Shchelkunov *et al.*, 1995)
		137		FPV	5.7e-45	60/127	47	(Senkevich *et al.*, 1997)
		377		VAR-I A16L (BSH:A17L)	1.4e-43	60/130	46	(Drillien *et al.*, 1987)
		378		VAC A16L	0.049	7/28	25	(Shchelkunov *et al.*, 1995)
					0.049	7/28	25	(Goebel *et al.*, 1990)
090R	78207	1286	146.9	RNA pol subunit rpo147				
J6R	82067	1286		VAC				(Broyles and Moss, 1986)
L6R		1286		VAR	0.0	1283/1286	99	(Goebel *et al.*, 1990)
MC079R		1289		MCV subtype I	0.0	1275/1286	99	(Shchelkunov *et al.*, 1995)
				100 matches to RNA pol (large subunit) family	0.0	556/760	73	(Senkevich *et al.*, 1997)
					<3.7e-07			
091L	82579	171	19.7	protein tyrosine/serine phosphatase				
	82064							(Rosel *et al.*, 1986)
H1L		171		VAC				(Guan *et al.*, 1991)
I11		171		VAR	2.0e-117	170/171	99	(Goebel *et al.*, 1990)
		171		racoonpox	1.1e-114	166/171	97	(Shchelkunov *et al.*, 1995)
		172		myxoma virus	6.0e-111	157/171	91	B47452
		173		rabbit fibroma virus	1.5e-77	83/138	60	(Mossman *et al.*, 1995a)
MC082L		169		MCV subtype I	1.8e-77	46/80	57	(Mossman *et al.*, 1995a)
				protein phosphatase family	1.4e-65	60/114	52	(Senkevich *et al.*, 1997)
					>2.8e-05			

ORF[a]	START STOP	AA[b]	kDa[c]	name / (putative) function / homologies[g]	BLAST[d] expect	BLAST[e] AA id	HSS[f] (%)	references
left terminal region:								
092R	82593	189	21.5	21.5k protein				(Rosel *et al.*, 1986)
H2R	83162	189		VAC	5.2e-134	188/189	99	(Goebel *et al.*, 1990)
I2R		189		VAR	1.4e-133	188/189	99	(Shchelkunov *et al.*, 1995)
MC083R		191		MCV subtype 1	1.4e-71	95/181	52	(Senkevich *et al.*, 1997)
		142		myxoma	1.3e-65	93/142	65	(Jackson and Bulls, 1990)
093L	84139 83165	324	37.5	immunodominant env protein p35; LMV membrane-associated				(Rosel *et al.*, 1986) (Chertov *et al.*, 1991) (Takahashi *et al.*, 1994)
H3L		324		VAC	3.3e-231	322/324	99	(Goebel *et al.*, 1990)
I3L		325		VAR-BSH	1.7e-225	311/320	97	(Shchelkunov *et al.*, 1995)
MC084L		298		MCV subtype 1	1.1e-36	38/117	32	(Senkevich *et al.*, 1996)
094L	86527 84140	795	93.6	RAP 94 (RNA-pol assoc. transcr. spec. factor)				(Ahn and Moss, 1992b) (Kane and Shuman, 1992)
H4L		795		VAC	0.0	791/795	99	(Goebel *et al.*, 1990)
I4L		795		VAR	0.0	780/795	98	(Shchelkunov *et al.*, 1995)
MC085L		791		MCV subtype 1	0.0	327/546	59	(Senkevich *et al.*, 1996)
		804		Orf virus	0.0	96/131	73	(Fleming *et al.*, 1993)
		484		FPV L1L protein	2.4e-181	91/176	51	2209386A
095R	86713 87324	203	22.3	late transcription factor VLTF-4				(Kovacs and Moss, 1996) (Rosel *et al.*, 1986)
H5R		203		VAC	1.8e-128	202/203	99	(Goebel *et al.*, 1990)
I5R		221		VAR	5.1e-102	91/97	93	(Shchelkunov *et al.*, 1995)
		227		orf virus F3R	3.1e-14	29/69	42	(Fleming *et al.*, 1993)
		220		MCV subtype 1	3.1e-09	28/64	43	(Senkevich *et al.*, 1997)
		705		nucleolin Xenopus	0.00041	18/57	31	(Messmer and Dreyer, 1993)
				31 matches to glu/asp rich proteins	E<0.52			
096R	87325 88269	314	36.7	DNA topoisomerase I				(Shuman and Moss, 1987) (Rosel *et al.*, 1986)
H6R		314		VAC	0.0	314/314	100	(Goebel *et al.*, 1990)
I6R		314		VAR-BSH	9.5e-220	312/314	99	(Shchelkunov *et al.*, 1995)
		314		shope fibroma virus	8.5e-141	119/170	70	(Upton *et al.*, 1990b)
		318		orf virus	5.2e-128	82/138	59	(Fleming *et al.*, 1993)
MC087R		323		MCV subtype 1	1.6e-121	111/202	54	(Senkevich *et al.*, 1997)
		316		FPV L3R	2.9e-113	159/303	52	(Zantinge *et al.*, 1996)
				21 matches to topoisomerase family				
097R	88306	146	17.0	17.0k protein				(Rosel *et al.*, 1986)
H7R	88746	146		VAC	2.1e-98	144/146	98	(Goebel *et al.*, 1990)
I7R		146		VAR	6.7e-96	141/146	96	(Shchelkunov *et al.*, 1995)
MC088R		143		MCV subtype 1	4.3e-30	45/115	39	(Senkevich *et al.*, 1997)
098R	88790 91324	844	96.8	mRNA capping enzyme, large subunit				(Morgan *et al.*, 1984) (Niles *et al.*, 1986)
D1R		844		VAC	0.0	842/844	99	(Goebel *et al.*, 1990)
F1R		844		VAR-BSH	0.0	830/844	98	(Shchelkunov *et al.*, 1995)
MC090R		950		MCV subtype 1	0.0	322/64	64	(Senkevich *et al.*, 1997)
		836		shope fibroma virus	0.0	243/305	79	(Upton *et al.*, 1991b)
		868		ASV NP868R	0.0033	17/55	30	(Pena *et al.*, 1993)
099L	91723 91283	146	16.9	structural protein				(Niles *et al.*, 1986) (Dyster and Niles, 1991)
D2L		146		VAC	5.9e-98	146/146	100	(Goebel *et al.*, 1990)
F2L		146		VAR (BSH: F3L)	1.5e-97	145/146	99	(Shchelkunov *et al.*, 1995)
		143		Rabbit fibroma virus	2.0e-27	13/33	39	(Upton *et al.*, 1991b)
MC091L		170		MCV subtype 1	1.1e-20	19/41	46	(Senkevich *et al.*, 1996)
100R	91716	233	27.6	27k structural protein				(Dyster and Niles, 1991)
D3R	92417	237		VAC	3.8-167	136/142	95	(Goebel *et al.*, 1990)
F2R		237		VAR I:F3R	1.5e-162	131/142	92	(Shchelkunov *et al.*, 1995)
		241		shope fibroma virus	9.3e-20	27/100	27	(Upton *et al.*, 1991b)
MC092R		268		MCV subtype 1	3.5e-18	16/39	41	(Senkevich *et al.*, 1997)
		206		rabbit fibroma virus C3	1.6e-09	26/96	27	(Strayer *et al.*, 1991)
101R	92417	218	25.1	uracil DNA glycosylase				(Upton *et al.*, 1993)
D4R	93073	218		VAC	1.4e-157	217/218	99	(Goebel *et al.*, 1990)
F4R		218		VAR-BSH	5.1e-157	216/218	99	(Shchelkunov *et al.*, 1995)
		218		shope fibroma virus	1.5e-117	151/218	69	(Upton *et al.*, 1993)
MC093R		226		MCV subtype 1	8.4e-91	65/113	57	(Senkevich *et al.*, 1997)
		218		FPV FPD4	3.1e-88	116/216	53	(Tartaglia *et al.*, 1990)
		297		uracil DNA glycosylase UL2 gallid herpesvirus 1	0.019	8/14	57	L34064
102R	93105 95462	785	90.4	90.4k ATP/GTP binding protein				(Niles *et al.*, 1986) (Shchelkunov *et al.*, 1993c)
D5R		785		VAC	0.0	780/785	99	(Goebel *et al.*, 1990)
F5R		785		VAR	0.0	774/785	98	(Shchelkunov *et al.*, 1995)
		786		shope fibroma C5	0.0	283/450	62	(Strayer *et al.*, 1991)
		791		MCV subtype 1	0.0	184/334	55	(Senkevich *et al.*, 1997)
		791		FPV virus FPD5	0.0	170/345	49	(Tartaglia *et al.*, 1990)
MC094R		942		C29E6.4 C. elegans	0.72	16/56	28	(Wilson *et al.*, 1994)
103R	95503 97416	637	73.9	early transcription factor VETF-1				(Broyles and Fesler, 1990) (Gershon and Moss, 1990)

GENOMIC SEQUENCE OF THE MVA STRAIN

ORF[a]	START STOP	AA[b]	kDa[c]	name / (putative) function / homologies[e]	BLAST[d] expect	BLAST[e] AA id	HSS[f] (%)	references
left terminal		region:						
D6R		637		VAC	0.0	635/637	99	(Goebel *et al.*, 1990)
F6R		637		VAR-1	0.0	633/637	99	(Shchelkunov *et al.*, 1995)
		635		shope fibroma virus	0.0	212/262	80	(Strayer *et al.*, 1991)
MC095R		635		MCV subtype 1	0.0	199/263	75	(Senkevich *et al.*, 1997)
		605		FPV	0.0	188/263	71	(Binns *et al.*, 1990)
		648		Choristoneura biennis EPV	2.7e-08	24/72	33	(Tartaglia *et al.*, 1990)
		648		Amsacta moorei EPV	4.2e-06	24/77	31	(Yuen *et al.*, 1991)
		706		African swine fever virus	1.5e-05	13/38	34	(Hall and Moyer, 1991)
								(Yanez *et al.*, 1993)
104R	97443 97928	161	17.9	**RNA polymerase subunit rpo18**				(Ahn *et al.*, 1990b)
D7R		161		VAC	1.4e-108	160/161	99	(Quick and Broyles, 1990)
F7R		161		VAR	2.2e-106	156/161	96	(Goebel *et al.*, 1990)
		163		rabbit fibroma C8	3.4e-76	108/161	67	(Shchelkunov *et al.*, 1995)
MC097R		161		MCV subtype 1	4.0e-70	99/158	62	(Strayer *et al.*, 1991)
		161		FPV D7	5.4e-66	95/160	59	(Senkevich *et al.*, 1997)
								(Binns *et al.*, 1990)
105L	98805 97891	304	35.4	**virion transmembrane protein, carbonic anhydrase-like**				(Niles and Seto, 1988)
								(Niles *et al.*, 1986)
D8L		304		VAC	2.3e-212	297/304	97	(Maa *et al.*, 1990)
F8L		304		VAR	2.5e-209	291/304	95	(Goebel *et al.*, 1990)
		304		Camelpox virus	1.1e-207	290/304	95	(Shchelkunov *et al.*, 1995)
		303		Ectromelia virus	2.2e-207	195/207	94	X97857
		304		Monkeypox virus	3.0e-207	287/304	94	X97856
		304		Cowpox virus	9.8e-206	285/304	93	X97855
				Carbonic anhydrase family	>4.9e-13			X97858
106R	98847 99488	213	25.0	**25k mutT-like protein**				(Koonin, 1993)
D9R		213		VAC	1.6e-146	212/213	99	(Niles *et al.*, 1986)
F9R		213		VAR	5.3e-145	209/213	98	(Goebel *et al.*, 1990)
		218		rabbit fibroma	1.7e-75	105/203	51	(Shchelkunov *et al.*, 1995)
MC098R		212		MCV subtype 1	5.3e-67	54/111	48	(Strayer *et al.*, 1991)
		78		FPV D9	2.0e-13	25/51	49	(Senkevich *et al.*, 1997)
MC099R		229		MCV subtype 1	0.0041	13/31	41	(Tartaglia *et al.*, 1990)
		248		VAR-1 F10R	0.018	14/32	43	(Senkevich *et al.*, 1997)
		225		FPV D10	0.14	15/34	44	(Shchelkunov *et al.*, 1995)
		248		VAC D10R	0.23	11/26	42	(Tartaglia *et al.*, 1990)
								(Goebel *et al.*, 1990)
107R	99485 100231	248	28.9	**29k mutT-like protein**				(Koonin, 1993)
D10R		248		VAC	7.4e-173	245/248	98	(Niles *et al.*, 1986)
F10R		248		VAR-1	5.4e-173	245/248	98	(Goebel *et al.*, 1990)
		260		shope fibroma D10	3.8e-72	96/202	47	(Shchelkunov *et al.*, 1995)
MC099R		229		MCV subtype 1	1.4e-54	44/100	44	(Strayer *et al.*, 1991)
		225		FPV D10	1.1e-45	45/102	44	(Senkevich *et al.*, 1997)
		218		shope fibroma D9	1.9e-06	19/54	35	(Binns *et al.*, 1990)
		212		MCV subtype 1 MC098R	0.13	12/21	57	(Strayer *et al.*, 1991)
		136		mutator Synechocystis	0.23	12/27	44	(Senkevich *et al.*, 1997)
		213		VAC D9R	0.24	11/26	42	D90899
		213		VAR F9R	0.24	11/26	42	(Goebel *et al.*, 1990)
		169		mutator M. jannaschii	0.39	13/25	52	(Shchelkunov *et al.*, 1995)
								(Bult *et al.*, 1996)
108L	102127 100232	631	72.4	**nucleoside triphosphate phosphohydrolase I, DNA helicase**				(Broyles and Moss, 1987)
D11L		631		VAC	0.0	629/631	99	(Rodriguez *et al.*, 1986)
N1L		631		VAR	0.0	626/631	99	(Koonin and Senkevich, 1992)
MC100R		634		MCV subtype 1	7.3e-286	392/627	62	(Goebel *et al.*, 1990)
		637		FPV protein 5	2.8e-275	214/357	59	(Shchelkunov *et al.*, 1995)
		370		Rabbit fibroma C14 protein	1.8e-176	244/368	66	(Senkevich *et al.*, 1996)
		648		AmEPV	6.0e-142	81/159	50	S42251
		648		Choristoneura biennis EPV	1.1e-136	81/158	51	F36819
		89		Swinepox virus	1.2e-34	60/89	67	(Hall and Moyer, 1991)
		1098		ASF	1.6e-13	26/89	29	(Yuen *et al.*, 1991)
		1085		RAD26 (yeast)	5.1e-05	16/45	35	(Massung *et al.*, 1993)
		769		HS transcription activator NTPase family	0.00093 >5.1e-5	10/22	45	(Baylis *et al.*, 1993) (Huang *et al.*, 1994) (Okabe *et al.*, 1992)
109L	103025 102162	287	33.3	**mRNA capping enzyme, transcription initiation factor VITF**				(Niles *et al.*, 1989)
D12L		287		VAC	2.0e-198	285/287	99	(Weinrich and Hruby, 1986)
N2L		287		VAR	9.8e-198	284/287	99	(Vos *et al.*, 1991)
-		287		Swinepox virus	4.1e-160	220/287	76	(Goebel *et al.*, 1990)
MC101L		295		MCV subtype 1	5.8e-126	171/279	61	(Shchelkunov *et al.*, 1995)
		289		FPV protein 6	3.4e-113	114/215	53	(Massung *et al.*, 1993)
								(Senkevich *et al.*, 1996)
								S42252
110L	104711 103056	551	61.9	**rifampicin resistance gene, IMV protein**				(Tartaglia and Paoletti, 1985)
D13L		551		VAC	0.0	551/551	100	(Weinrich and Hruby, 1986)
N3L		551		VAR	0.0	547/551	99	(Goebel *et al.*, 1990)
		551		Swinepox virus	4.5e-286	357/506	70	(Shchelkunov *et al.*, 1995)
MC102L		547		MCV subtype 1	5.4e-248	298/494	60	(Massung *et al.*, 1993)
		552		FPV protein 7	6.6e-223	182/305	59	(Senkevich *et al.*, 1996)
		584		Heliothis armigera EPV	9.5e-51	54/107	50	S42253
								(Osborne *et al.*, 1996)

ORF[a]	START STOP	AA[b]	kDa[c]	name / (putative) function / homologies[e]	BLAST[d] expect	BLAST[e] AA id	HSS[f] (%)	references
left terminal region:								
111L	105187	150	16.9	late gene trans-activator, VLTF-2				(Weinrich and Hruby, 1986)
	104735							(Keck *et al.*, 1993)
A1L		150		VAC	6.8e-103	149/150	99	(Goebel *et al.*, 1990)
A1L		150		VAR	6.8e-103	149/150	99	(Shchelkunov *et al.*, 1995)
MC103L		169		MCV subtype 1	6.3e-54	74/147	50	(Senkevich *et al.*, 1996)
		154		FPV protein 8	2.8e-50	50/87	57	S42254
112L	105882	224	26.3	late gene trans-activator				(Weinrich and Hruby, 1986)
A2L	105208			VAC				(Passarelli *et al.*, 1996)
A2L		224		VAR	1.3e-158	224/224	100	(Goebel *et al.*, 1990)
MC104L		224		MCV subtype 1	1.3e-158	224/224	100	(Shchelkunov *et al.*, 1995)
		228		orf virus	6.4e-127	172/222	77	(Senkevich *et al.*, 1996)
		606			6.8e-30	43/66	65	(Mercer *et al.*, 1995)
113L	106109	76	8.9	8.9k protein				
	105879	76		VAC-WR	1.6e-47	73/76	96	(Weinrich and Hruby, 1986)
A3L		76		VAR-BSH (I:A2.5L)	2.1e-47	71/76	93	(Shchelkunov *et al.*, 1995)
MC105L		70		MCV subtype 1	9.8e-12	26/63	41	(Senkevich *et al.*, 1996)
114L	108058	644	72.6	major core protein P4b				(Rosel and Moss, 1985)
A3L	106124	644		VAC	0.0	643/644	99	(Goebel *et al.*, 1990)
A4L		644		VAR-BSH (I:A3L)	0.0	636/644	98	(Shchelkunov *et al.*, 1995)
MC106L		675		MCV subtype 1	8.9e-272	227/357	63	(Senkevich *et al.*, 1996)
		657		FPV Major core protein P4b	9.1e-220	169/299	56	(Binns *et al.*, 1989)
115L	108929	272	29.9	membrane associated core protein				(Demkowicz *et al.*, 1992)
	108111							(Cudmore *et al.*, 1996)
A4L		281		VAC	1.1e-145	180/187	96	(Goebel *et al.*, 1990)
A5L		271		VAR-BSH (I: A4L)	1.1e-112	165/178	92	(Shchelkunov *et al.*, 1995)
		268		Thermoproteus phage 1	1.9e-09	38/127	29	(Neumann and Zillig, 1990)
		5179		human mucin	4.5e-07	34/139	24	(Gum *et al.*, 1994)
				many matches to Pro-rich proteins				
116R	108967	164	19.0	RNA pol subunit rpo19				(Ahn *et al.*, 1992)
A5R	109461	164		VAC	5.8e-110	164/164	100	(Goebel *et al.*, 1990)
A5R		164		VAR-I (BSH:A6R)	7.0e-109	162/164	98	(Shchelkunov *et al.*, 1995)
MC108R		165		MCV subtype 1	3.3e-51	82/151	53	(Senkevich *et al.*, 1997)
		167		FPV	3.3e-51	72/161	44	(Kumar and Boyle, 1990)
				54 matches/glu-rich proteins	<0.51			
117L	110576	372	43.1	43.1k protein				
A6L	109458	372		VAC	1.2e-248	371/372	99	(Goebel *et al.*, 1990)
A7L		372		VAR-BSH (I: A6L)	1.1e-244	364/372	97	(Shchelkunov *et al.*, 1995)
MC109L		461		MCV subtype 1	4.0e-99	132/367	35	(Senkevich *et al.*, 1996)
		339		FPV ORF 2 protein	1.9e-95	111/279	39	B60013
118L	112732	710	82.3	VETF 82k subunit				(Gershon and Moss, 1990)
A7L	110600	710		VAC	0.0	708/710	99	(Goebel *et al.*, 1990)
A8L		710		VAR-BSH (I: A7L)	0.0	700/710	98	(Shchelkunov *et al.*, 1995)
MC110L		707		MCV subtype 1	0.0	240/374	64	(Senkevich *et al.*, 1996)
119R	112786	288	33.6	33.6k protein				(Van Meir and Wittek, 1988)
A8R	113652	288		VAC	5.3e-198	287/288	99	(Goebel *et al.*, 1990)
A8R		288		VAR-I (BSH:A9R)	3.1e-195	284/288	98	(Shchelkunov *et al.*, 1995)
MC111R		435		MCV subtype 1	4.4e-94	100/169	59	(Senkevich *et al.*, 1997)
120L	113929	94	10.5	10.5k protein				(Van Meir and Wittek, 1988)
A10L	113645	95		VAR-BSH (I: A9L)	9.0e-59	78/79	98	(Shchelkunov *et al.*, 1995)
A9L		99		VAC	9.4e-55	82/91	90	(Goebel *et al.*, 1990)
MC112L		128		MCV subtype 1	1.0e-29	47/71	66	(Senkevich *et al.*, 1996)
		69		orf virus	3.0e-16	27/45	60	(Mercer *et al.*, 1995)
121L	116605	891	102.2	major core protein P4a				(Van Meir and Wittek, 1988)
	113930							(Vanslyke *et al.*, 1991)
A10L		891		VAC	0.0	883/891	99	(Goebel *et al.*, 1990)
A11L		892		VAR-BSH (I: A10L)	0.0	442/463	95	(Shchelkunov *et al.*, 1995)
MC113L		889		MCV subtype 1	5.8e-289	99/177	55	(Senkevich *et al.*, 1996)
122R	116620	318	36.1	36.1k protein				(Goebel *et al.*, 1990)
A11R	117576	318		VAC	3.5e-212	318/318	100	(Goebel *et al.*, 1990)
A11R		319		VAR-I (BSH: A12R)	2.7e-154	242/277	87	(Shchelkunov *et al.*, 1995)
MC114R		304		MCV subtype 1	2.9e-98	92/154	59	(Senkevich *et al.*, 1997)
		148		FPV 4a gene	1.9e-13	18/32	56	A20158
123L	118141	187	20.0	virion protein				(Takahashi *et al.*, 1994)
A12L	117578	192		VAC	4.8e-127	127/128	99	(Goebel *et al.*, 1990)
A13L		189		VAR-BSH (I: A12L)	5.9e-64	101/144	70	(Shchelkunov *et al.*, 1995)
MC115L		178		MCV subtype 1	5.9e-37	39/83	46	(Senkevich *et al.*, 1996)
124L	118377	70	7.6	structural protein				(Takahashi *et al.*, 1994)
	118165			IMV membrane protein				(Jensen *et al.*, 1996)
		70		p8	2.4e-42	66/69	95	(Goebel *et al.*, 1990)
A13L		68		VAC	4.1e-20	37/64	57	(Shchelkunov *et al.*, 1995)
A14L				VAR-BSH (I: A13L)				
125L	118757	90	10.0	structural protein				(Takahashi *et al.*, 1994)
	118485			IMV membrane protein p16				(Jensen *et al.*, 1996)

GENOMIC SEQUENCE OF THE MVA STRAIN

ORF[a]	START STOP	AA[b]	kDa[c]	name / (putative) function / homologies[e]	BLAST[d] expect	BLAST[e] AA id	HSS[f] (%)	references
left terminal region:								
A14L		90		VAC	5.3e-62	90/90	100	(Goebel *et al.*, 1990)
A15L		90		VAR-BSH (l: A14L)	5.3e-61	88/90	97	(Shchelkunov *et al.*, 1995)
MC118L		94		MCV subtype 1	7.3e-22	31/72	43	(Senkevich *et al.*, 1996)
		125		human interferon inducible protein	0.23	15/49	30	(Deblandre *et al.*, 1995)
126L	119209	94	11.0	11k protein				
A15L	118925	94		VAC	4.1e-63	94/94	100	(Goebel *et al.*, 1990)
A16L		94		VAR-BSH (l:A15L)	1.0e-61	92/94	97	(Shchelkunov *et al.*, 1995)
MC120L		96		MCV subtype 1	6.7e-08	17/51	33	(Senkevich *et al.*, 1996)
127L	120326	377	43.4	35k myristylprotein				(Martin *et al.*, 1997)
A16L	119193	378		VAC	6.3e-288	327/327	100	(Goebel *et al.*, 1990)
A17L		377		VAR-BSH (l:A16L)	1.5e-283	368/377	97	(Shchelkunov *et al.*, 1995)
MC121L		364		MCV subtype 1	6.5e-110	45/115	39	(Senkevich *et al.*, 1996)
128L	120940 120329	203	23.0	IMV membrane protein morphogenesis factor				(Krijnse-Locker *et al.*, 1996) (Rodriguez *et al.*, 1995) (Wolffe *et al.*, 1996)
A17L		203		VAC	1.0e-141	201/203	99	(Goebel *et al.*, 1990)
A18L		203		VAR-BSH (l:A17L)	1.0e-141	201/203	99	(Shchelkunov *et al.*, 1995)
MC122L		179		MCV subtype 1	1.4e-47	36/81	44	(Senkevich *et al.*, 1996)
129R	120955 122436	493	56.8	DNA helicase DNA dependent ATPase				(Koonin and Senkevich, 1992) (Bayliss and Condit, 1995)
A18R		493		VAC	0.0	488/493	98	(Goebel *et al.*, 1990)
A18R		493		VAR-I (BSH:A19R)	0.0	478/493	96	(Shchelkunov *et al.*, 1995)
MC123R		694		MCV subtype 1	5.3e-167	203/403	50	(Senkevich *et al.*, 1997)
		450		Bacteriophage T5 D10 helicase-like protein	0.0066	13/36	36	P11107
130L	122650	77	8.3	8.3kb protein				(Goebel *et al.*, 1990)
A19L	122417	77		VAC	2.9e-50	77/77	100	(Goebel *et al.*, 1990)
A19L		76		VAR-I (BSH: A20L)	1.2e-34	54/64	84	(Shchelkunov *et al.*, 1995)
MC124L		78		MCV subtype 1	1.5e-13	14/37	37	(Senkevich *et al.*, 1996)
		1721		HS RIZ, zink finger protein	0.0060	7/16	43	(Buyse *et al.*, 1995)
131L	123004	117	13.6	13.6k protein				(Goebel *et al.*, 1990)
A21L	122651	117		VAC	5.3e-83	117/117	100	(Goebel *et al.*, 1990)
A22L		117		VAR-BSH (l: A20L)	7.2e-82	115/117	98	(Shchelkunov *et al.*, 1995)
MC125L		114		MCV subtype 1	2.8e-28	23/41	56	(Senkevich *et al.*, 1996)
132R	123003	426	49.1	49.1k protein				(Goebel *et al.*, 1990)
A20R	124283	426		VAC	7.6e-298	423/426	99	(Goebel *et al.*, 1990)
A21R		426		VAR	1.6e-294	418/426	98	(Shchelkunov *et al.*, 1995)
MC126R		476		MCV subtype 1	3.2e-95	34/131	25	(Senkevich *et al.*, 1997)
		1118		Pichia klyveri DNA pol	0.069	12/54	22	Y11606
133R	124213	187	21.9	21.9k protein				(Goebel *et al.*, 1990)
A22R	124776	187		VAR-I (BSH:A23R)	1.1e-126	182/187	97	(Shchelkunov *et al.*, 1995)
A22R		176		VAC	1.2e-122	174/176	98	(Goebel *et al.*, 1990)
MC127R		282		MCV subtype 1	5.8e-43	35/85	41	(Senkevich *et al.*, 1997)
134R	124796	382	44.6	44.6k protein				(Goebel *et al.*, 1990)
A23R	125944	382		VAC	4.2e-269	382/382	100	(Goebel *et al.*, 1990)
A23R		382		VARI (BSH:A24R)	1.7e-265	377/382	98	(Shchelkunov *et al.*, 1995)
MC128R		383		MCV subtype 1	3.5e-136	83/143	58	(Senkevich *et al.*, 1997)
135R	125966 129436	1155	132.4	RNA pol subunit rpo132				(Hooda-Dhingra *et al.*, 1990) (Amegadzie *et al.*, 1991b)
A24R		1164		VAC	0.0	794/796	99	(Goebel *et al.*, 1990)
		1164		CPX rpo132	0.0	794/795	99	(Patel and Pickup, 1989)
A25R		1164		VAR-BSH (l:A24R)	0.0	789/795	99	(Shchelkunov *et al.*, 1995)
MC129R		1165		MCV subtype 1	0.0	441/565	78	(Senkevich *et al.*, 1997)
		1162		orf virus	0.0	166/258	64	U33419
				101 matches to RNA pol beta subunit family	<0.036			
right terminal region:								
136L	129638	65	7.5	150k CPX-ATI (f)				(Funahashi *et al.*, 1988)
A25L	129441	65		VAC	1.3e-41	64/65	98	(Goebel *et al.*, 1990)
		1284		Cowpox (CPX-ATI)	3.2e-15	28/30	93	(Funahashi *et al.*, 1988)
137L	130916	230	27.1	27.1k protein (f)				(Amegadzie *et al.*, 1991a)
A30L	130224	498		VAR-BSH (l: A29L)	3.1e-158	216/227	95	(Shchelkunov *et al.*, 1995)
A26L		322		VAC (ATI flanking protein)	5.6e-142	195/197	98	(Goebel *et al.*, 1990)
MC131L		513		MCV subtype 1	2.1e-12	19/59	32	(Senkevich *et al.*, 1996)
MC133L		546		MCV subtype 1	4.2e-11	12/40	30	(Senkevich *et al.*, 1996)
MC130L		451		MCV subtype 1	2.3e-10	14/40	35	(Senkevich *et al.*, 1996)
		702		VAR-I A28L (BSH:A29L)	0.0021	12/37	32	(Shchelkunov *et al.*, 1995)
		726		Camelpox	0.051	11/37	29	(Meyer and Rziha, 1993)
138L	131298 130966	110	12.5	14k membrane protein EEV protein fusion protein				(Rodriguez and Esteban, 1987) (Rodriguez and Smith, 1990) (Gong *et al.*, 1990)
A27L		110		VAC	3.3e-70	108/110	98	(Goebel *et al.*, 1990)
A31L		110		VAR-BSH (l: /A30L)	1.1e-69	107/110	97	(Shchelkunov *et al.*, 1995)
		117		Camelpox virus	1.5e-69	106/110	96	(Meyer *et al.*, 1994)
		110		Cowpox virus	1.6e-69	107/110	97	(Meyer *et al.*, 1994)

ORF[a]	START STOP	AA[b]	kDa[c]	name / (putative) function / homologies[g]	BLAST[d] expect	BLAST[e] AA id	HSS[f] (%)	references
left terminal region:								
		110		Ectromelia virus	6.7e-68	105/110	95	(Meyer *et al.*, 1994)
		110		Monkeypox virus	8.3e-67	103/110	93	(Meyer *et al.*, 1994)
		89		Orf virus	4.8e-15	22/57	38	(Nnase *et al.*, 1991)
		188		Myxoma virus	2.5e-12	18/33	54	(Jackson *et al.*, 1996)
MC133L		546		MCV subtype 1	1.5e-11	26/58	44	(Senkevich *et al.*, 1996)
		148		Capripox virus HM2 protein	2.6e-10	21/42	50	(Gershon *et al.*, 1989)
MC131L		513		MCV subtype 1	1.5e-05	18/58	31	(Senkevich *et al.*, 1996)
139L	131739	146	16.3	16.3k protein				
A28L	131299	146		VAC	1.7e-103	146/146	100	(Amegadzie *et al.*, 1991a)
A31.5L		146		VAR-BSH (I: A31L)	2.9e-100	141/146	96	(Goebel *et al.*, 1990)
		140		Myxoma virus	1.3e-55	30/52	57	(Shchelkunov *et al.*, 1995)
		140		Capripox virus HM3 protein	3.3e-55	30/49	61	(Jackson *et al.*, 1996)
MC134L		141		MCV subtype 1	1.0e-53	31/52	59	(Gershon *et al.*, 1989)
		143		Amsacta moorei poxvirus	2.0e-14	16/36	44	(Senkevich *et al.*, 1996)
140L	132657	305	35.4	RNA pol subunit rpo35				(Hall and Moyer, 1991)
A29L	131740	305		VAC	3.6e-215	304/305	99	(Amegadzie *et al.*, 1991a)
A32L		305		VAR-BSH	7.5e-211	297/305	97	(Goebel *et al.*, 1990)
MC135L		303		MCV subtype 1	7.0e-98	51/103	49	(Shchelkunov *et al.*, 1995)
		126		Capripox virus	2.2e-54	46/61	75	(Senkevich *et al.*, 1996)
141L	132853	77	8.7	8.7k protein				(Gershon *et al.*, 1989)
A30L	132620	77		VAC	5.5e-48	77/77	100	(Amegadzie *et al.*, 1991a)
A33L		77		VAR	5.5e-48	77/77	100	(Goebel *et al.*, 1990)
MC136L		67		MCV subtype 1	9.2e-16	18/40	45	(Shchelkunov *et al.*, 1995)
142R	133013	125	14.4	14.4k protein				(Senkevich *et al.*, 1996)
A31R	133390	124		VAC	2.0e-84	118/124	95	(Smith *et al.*, 1991)
A34R		140		VAR	1.6e-79	111/114	97	(Goebel *et al.*, 1990)
MC138R		117		MCV subtype 1	6.2e-24	39/98	39	(Shchelkunov *et al.*, 1995)
143L	134169	269	30.8	30.8k protein				(Senkevich *et al.*, 1997)
	133360			ATP/GTP binding motif A				(Smith *et al.*, 1991)
A32L		300		VAC	6.4e-190	268/269	99	(Koonin *et al.*, 1993)
A35L		270		VAR	1.6e-186	263/269	97	(Goebel *et al.*, 1990)
MC140L		249		MCV subtype 1	7.6e-95	58/94	61	(Shchelkunov *et al.*, 1995)
144R	134287	185	20.6	EEV glycoprotein				(Senkevich *et al.*, 1996)
A33R	134844	185		VAC	2.1e-124	182/185	98	(Roper *et al.*, 1996)
A36R		184		VAR	1.8e-121	103/112	91	(Goebel *et al.*, 1990)
		185		Ectromelia	2.8e-113	*165/185*	89	(Shchelkunov *et al.*, 1995)
145R	134868	168	19.6	EEV glycoprotein				(Roper *et al.*, 1996)
	135374			virulence factor				(Duncan and Smith, 1992a)
				actin microvilli inducer				(McIntosh and Smith, 1996)
A34R		168		VAC	1.2e-117	165/168	98	(Wolffe *et al.*, 1997)
A37R		168		VAR-I	1.7e-117	164/168	97	(Goebel *et al.*, 1990)
		167		FPV ORFs BamHI 2,8,11 hepatic lectins homologs	<0.056	16/66	24	(Shchelkunov *et al.*, 1995)
		199		HS early T-cell activation antigen CD69	0.0038	12/38	31	(Tomley *et al.*, 1988)
MC143R		159		MCV subtype 1	0.080	12/48	25	(Hamann *et al.*, 1993)
				17 matches to lectins				(Senkevich *et al.*, 1997)
146R	135418	176	20.0	20.0k protein				
A35R	135948	176		VAC	1.4e-126	176/176	100	(Smith *et al.*, 1991)
A38R		60		VAR-I	2.9e-37	57/60	95	(Goebel *et al.*, 1990)
MC145R		233		MCV subtype 1	1.2e-07	18/55	32	(Shchelkunov *et al.*, 1995)
147R	136015	208	23.8k	EEV membrane protein				(Senkevich *et al.*, 1997)
	136641			virulence factor				(Parkinson and Smith, 1994)
A36R		221		VAC	2.8e-143	140/141	99	(Smith *et al.*, 1991)
A39R		216		VAR	2.1e-89	138/177	77	(Goebel *et al.*, 1990)
				19 matches to asn/ser-rich proteins	<0.41			(Shchelkunov *et al.*, 1995)
148R	136705	263	29.8	29.8k protein				
A37R	137496	263		VAC	6.8e-183	261/262	99	(Goebel *et al.*, 1990)
A40R		68		VAR	4.9e-37	61/67	91	(Shchelkunov *et al.*, 1995)
149L	138589	277	31.5	31.5k protein				
A38L	137756	277		VAC	9.3e-198	274/277	98	(Amegadzie *et al.*, 1991a)
A41L		277		VAR	1.6e-187	259/277	93	(Goebel *et al.*, 1990)
		303		Rattus norvegicus CD47	3.9e-24	23/86	26	(Shchelkunov *et al.*, 1995)
		324		MM integrin assoc. protein	1.0e-21	23/86	26	(Nishiyama *et al.*, 1997)
		323		human CD47 precursor	5.0e-19	28/86	32	(Lindberg *et al.*, 1993)
								(Campbell *et al.*, 1992)
150R	138606	83	9.4	semaphorin-like protein (f1)				(Kolodkin *et al.*, 1993)
	138857							
A39R		403		VAC	8.0e-46	73/76	96	(Goebel *et al.*, 1990)
A42R		74		VAR-I	8.6e-44	67/71	94	(Shchelkunov *et al.*, 1995)
151R	139163	210	23.9	semaphorin-like protein (f2)				(Kolodkin *et al.*, 1993)
	139795							
A39R		403		VAC	3.0-147	209/210	99	(Goebel *et al.*, 1990)
A43R		139		VAR (I:A44R)	1.8e-68	91/105	86	(Shchelkunov *et al.*, 1995)
		653		semaphorin-like protein Alcelaphine herpesvirus	1.7e-20	29/79	36	(Ensser and Fleckenstein, 1995)
				37 matches to semaphorin				

GENOMIC SEQUENCE OF THE MVA STRAIN

ORF[a]	START STOP	AA[b]	kDa[c]	name / (putative) function / homologies[e]	BLAST[d] expect	BLAST[e] AA id	HSS[f] (%)	references
left terminal region:								
				/collapsin gene family				
152R	139821 140327	168	19.4	NK cell receptor homolog lectin-like protein				(Scheiflinger et al., unpubl.) (Smith *et al.*, 1991)
A40R		168		VAC	6.6e-97	134/137	97	(Goebel *et al.*, 1990)
A45R		61		VAR-I (BSH: A43.5R)	9.6e-36	54/59	91	(Shchelkunov *et al.*, 1995)
		233		HS natural killer (NK) cell protein group 2-A, B	4.5e-11	20/74	27	(Houchins *et al.*, 1991)
		240		HS type II membrane protein	6.9e-11	16/36	44	(Adamkiewicz *et al.*, 1994)
		182		MM NK cell receptor	5.5e-09	16/36	44	(Giorda *et al.*, 1992)
		179		HS CD 94	1.7e-07	11/29	37	(Chang *et al.*, 1995a)
				127 matches to lectins including NK cell surface proteins and snake venoms				
153L	141025	219	25.1	25.1k protein				(Smith *et al.*, 1991)
A41L	140366	219		VAC	1.9e-158	218/219	99	(Goebel *et al.*, 1990)
A44L		218		VAR-BSH (I:A46L)	1.4e-152	152/159	95	(Shchelkunov *et al.*, 1995)
		244		VAC B29R/C23L	0.0076	12/53	22	(Goebel *et al.*, 1990)
		258		Rabbit fibroma virus T1	0.057	13/49	26	(Upton *et al.*, 1987)
154R	141197 141583	128	14.5	profilin-like protein				(Blasco *et al.*, 1991)
A42R		133		VAC	1.2e-87	85/87	97	(Smith *et al.*, 1991)
A47R		133		VAR-I (BSH:A45R)	1.4e-85	82/87	94	(Goebel *et al.*, 1990)
		140		HS profilin	2.2e-23	19/45	42	(Shchelkunov *et al.*, 1995)
				10 matches profilin family				(Kwiatkowski and Bruns, 1988)
155R	141621 142193	190	22.1	class I membrane glycoprotein				(Smith *et al.*, 1991)
A43R		194		VAC	1.5e-137	162/164	98	(Duncan and Smith, 1992b)
A48R		195		VAR-I (BSH:A46R)	1.9e-128	101/109	92	(Goebel *et al.*, 1990)
		51		HS leukocyte antigen	0.096	7/23	30	(Shchelkunov *et al.*, 1995) X79517
156R	142201	78	8.8	8.8k protein				
	142437	78		VAC-WR SalF6R	3.9e-45	78/78	100	(Smith *et al.*, 1991)
		258		rabbit myosin heavy chain	0.00048	13/39	33	(Smith *et al.*, 1991) A02985
				144 matches to various asp/glu/lys-rich proteins				
157L	143577 142537	346	39.4	3ß-hydroxysteroid dehydrogenase (3ß-HSD)				(Moore and Smith, 1992)
A44L		346		VAC	4.5e-249	342/346	98	(Blasco *et al.*, 1991)
A47L		210		VAR-BSH (I: A49L)	1.1e-136	185/195	94	(Goebel *et al.*, 1990)
MC152R		354		MCV subtype 1	8.2e-104	123/272	45	(Shchelkunov *et al.*, 1995)
		369		FPV	3.1e-83	33/85	38	(Senkevich *et al.*, 1996)
				matches to dihydroflavonol reductases, cholesterol dehydrogenases, UDP-galactose-4-epimerases	>2.8e-05			(Skinner *et al.*, 1994) (Baker and Blasco, 1992)
158R	143624 143989	121	13.3	superoxide dismutase-like protein				(Blasco *et al.*, 1991)
A45R		125		VAC	2.1e-82	94/96	97	(Smith *et al.*, 1991)
A51R		125		VAR-I BSH A48R	1.1e-82	93/96	96	(Goebel *et al.*, 1990)
				117 matches with superoxide dismutase family	<0.027			(Shchelkunov *et al.*, 1995)
159R	143979	241	27.6	27.6k protein				(Smith *et al.*, 1991)
A46R	144701	214		VAC	9.6e-167	238/240	99	(Goebel *et al.*, 1990)
A52R		240		VAR-I (BSH: A49R)	5.6e-164	233/240	97	(Shchelkunov *et al.*, 1995)
160L	145465	238	27.6	27.6k protein				(Goebel *et al.*, 1990)
J1L	144749	244		VAR	5.1e-146	114/127	89	(Shchelkunov *et al.*, 1995)
A47L		244		VAC	8.2e-135	121/127	95	(Goebel *et al.*, 1990)
				integrin lipid binding motif				(Smith *et al.*, 1991)
161R	145564	204	23.2	thymidylate kinase				(Smith *et al.*, 1991)
A48R	146178	204		VAC	5.2e-140	204/204	100	(Goebel *et al.*, 1990)
J2R		205		VAR	1.1e-137	161/165	97	(Shchelkunov *et al.*, 1995)
				16 matches to thymidylate kinase family	<0.49			
162R	146202	162	18.8	18.8k protein				(Smith *et al.*, 1991)
A49R	146690	162		VAC	6.0e-106	159/162	98	(Goebel *et al.*, 1990)
J3R		162		VAR	2.4e-103	154/162	95	(Shchelkunov *et al.*, 1995)
163R	146722	552	63.5	DNA ligase				(Kerr and Smith, 1989)
A50R	148380	552		VAC	0.0	547/552	99	(Goebel *et al.*, 1990)
J4R		552		VAR-I	0.0	537/552	97	(Shchelkunov *et al.*, 1995)
		922		HS DNA ligase III	2.1e-235	102/165	61	(Wei *et al.*,)
		559		shope fibroma ligase	9.9e-213	95/200	47	(Parks *et al.*, 1994)
		564		FPV ligase	3.0e-195	101/170	59	(Skinner *et al.*, 1994)
				31 matches mainly to DNA ligase family	<0.029			
164R	148426	310	34.9	34.9k protein				(Antoine *et al.*, 1996)
A51R	149358	334		VAC	1.5e-217	267/274	97	(Goebel *et al.*, 1990)
J5R		334		VAR	9.1e-208	251/274	91	(Shchelkunov *et al.*, 1995)

ORF[a]	START STOP	AA[b]	kDa[c]	name / (putative) function / homologies[g]	BLAST[d] expect	BLAST[e] AA id	HSS[f] (%)	references
left terminal region:								
				fusion of *A51R/A55R* ORFs				(Antoine *et al.*, 1996)
165R	149416	315	34.8	hemagglutinin				(Shida, 1986)
A56R	150363	315		VAC	1.8e-211	312/315	99	(Goebel *et al.*, 1990)
J9R		313		VAR-I(BSH:J7R)	4.3e-178	183/238	76	(Shchelkunov *et al.*, 1995)
		310		raccoonpox	1.5e-91	74/104	71	(Cavallaro and Esposito, 1992)
				124 matches to various proteins	<0.34			
166R	150659	97	11.4	guanylate kinase (f)				(Smith *et al.*, 1991)
A57R	150952	151		VAC	3.2e-62	94/97	96	(Goebel *et al.*, 1990)
J10R		151		VAR (BSH:J8R)	2.2e-57	88/97	90	(Shchelkunov *et al.*, 1995)
		198		MM guanylate kinase	4.3e-24	39/91	42	(Brady *et al.*, 1996)
		197		HS guanylate kinase	2.8e-20	35/91	38	(Brady *et al.*, 1996)
				21 matches mainly to guanylate kinases	<0.20			
167R	151103 152005	300	34.3	serine/threonine protein kinase				(Howard and Smith, 1989) (Banham and Smith, 1992) (Lin *et al.*, 1992)
B1R		300		VAC	7.1e-215	298/300	99	(Goebel *et al.*, 1990)
B1R		300		VAR-I	2.7e-210	289/300	96	(Shchelkunov *et al.*, 1995)
		283		VAC B12R	4.9e-49	27/53	50	(Goebel *et al.*, 1990)
				100 matches mainly to protein kinase family	<0.00031			
168R	152144	96	11.5	24.6k protein (f1)				
B2R	152434	219		VAC	8.5e-38	54/60	90	(Goebel *et al.*, 1990)
		149		histone H2A pea	0.59	16/50	32	P40281
169R	152289	143	16.1	24.6k protein (f2)				(Goebel *et al.*, 1990)
B2R	152720	219		VAC	5.7e-86	124/128	96	(Goebel *et al.*, 1990)
170R	152917	179	20.9	20.9k protein (f)				
B3R	153456	124		VAC	8.2e-33	51/56	91	(Goebel *et al.*, 1990)
		167		VAC WR	5.3e-45	51/56	91	(Smith *et al.*, 1991)
		92		VAR-GAR H5R	3.4e-06	19/28	67	U18339
171R	153683 154216	177	21.4	65k ank-like protein virulence factor (f1)				(Howard *et al.*, 1991) (Mossman *et al.*, 1996)
B4R		558		VAC	8.5e-107	151/154	98	(Goebel *et al.*, 1990)
B6R		558		VAR-I (BSH:B5R)	1.7e-98	140/154	90	(Shchelkunov *et al.*, 1995)
172R	154107 155336	409	47.7	65k ank-like protein virulence factor (f2)				(Howard *et al.*, 1991) (Mossman *et al.*, 1996)
B4R		558		VAC	2.4e-283	195/201	97	(Goebel *et al.*, 1990)
B6R		558		VAR-I (BSH:B5R)	2.3e-270	185/201	92	(Shchelkunov *et al.*, 1995)
		483		MYX M-T5 protein	5.5e-10	19/57	33	(Mossman *et al.*, 1996)
		1765		MM ankyrin 3	9.7e-10	22/54	40	(Peters *et al.*, 1995)
		516		orf virus	1.8e-09	16/47	34	U34774
		574		VAC B18R	3.3e-09	11/23	47	(Goebel *et al.*, 1990)
		574		VAR-I B19R	3.6e-09	19/72	26	(Shchelkunov *et al.*, 1995)
		882		HS KIAA0379	5.1e-09	20/52	38	AB002377
		668		CPX host range gene	1.7e-08,	14/47	29	(Spehner *et al.*, 1988)
		237		VAC WR hr gene	2.8e-08	15/47	31	(Kotwal and Moss, 1988a)
		472		VAC M1L	5.1e-07	23/81	28	(Goebel *et al.*, 1990)
		474		CPX O1L	8.7e-07	22/61	36	(Safronov *et al.*, 1996)
		446		VAR O1L	8.8e-07	23/81	28	(Shchelkunov *et al.*, 1995)
		437		CPX D1L	1.7e-06	8/27	29	(Safronov *et al.*, 1996)
		634		VAC C9L	7.8e-05			(Goebel *et al.*, 1990)
				159 matches including ankyrin proteins				
173R	155424 156377	317	35.1	ps/hr protein/ EEV gp42 complement control protein				(Takahashi-Nishimaki *et al.*, 1991) (Engelstad *et al.*, 1992) (Isaacs *et al.*, 1992)
B5R		317		VAC	1.6e-232	312/317	98	(Goebel *et al.*, 1990)
B7R		317		VAR-I (BSH:B6R)	7.1e-220	294/316	93	(Shchelkunov *et al.*, 1995)
		259		CPX D17L	2.1e-12	16/52	30	(Safronov *et al.*, 1996)
				186 matches to complement control protein family	<7.7e-05			
174R	156474	173	20.2	20.2k protein				
B6R	156995	173		VAC	1.5e-121	173/173	100	(Goebel *et al.*, 1990)
B7R		65		VAR-BSH (I:B8R)	6.0e-40	62/65	95	(Shchelkunov *et al.*, 1995)
		685		NAD-protein ADP ribosyl-transferase phage T4	0.56	17/56	30	SXBPT4
175R	157033	177	20.7	20.7k protein				
B7R	157566	182		VAC	7.8e-129	95/108	87	(Goebel *et al.*, 1990)
		184		VAC C8L	0.16	9/44	20	(Goebel *et al.*, 1990)
		182		CPX D12L	0.49	8/36	22	(Safronov *et al.*, 1996)
				EF-hand calcium-binding domain				
176R	157621 158301	226	26.0	31k interferon-gamma receptor (f)				(Upton *et al.*, 1992) (Alcami and Smith, 1995)
B8R		272		VAC	3.3e-164	116/123	94	(Goebel *et al.*, 1990)
B8R		266		VAR-BSH (I:B9R)	3.0e-153	111/123	90	(Shchelkunov *et al.*, 1995)
		266		ECT	2.6e-151	110/123	89	(Mossman *et al.*, 1995b)
		274		swinepox C6	3.2e-09	12/31	38	(Massung *et al.*, 1993)

ORF[a]	START STOP	AA[b]	kDa[c]	name / (putative) function / homologies[e]	BLAST[d] expect	BLAST[e] AA id	HSS[f] (%)	references
left terminal region:								
177R	158458	72	8.3	8.3k protein				
B9R	158676	77		VAC	3.0e-49	60/60	100	(Goebel *et al.*, 1990)
		240		capripox T4 protein	1.2e-09	16/44	36	M28823
		237		shope fibroma virus	0.0057	15/50	30	F43692
178R	158639	158	17.9	17.9k protein				
B10R	159115	166		VAC	4.7e-110	146/146	100	(Goebel *et al.*, 1990)
		530		swinepox VC04	0.040	13/42	30	(Massung *et al.*, 1993)
		689		kelch protein D. melanogaster	0.14	12/54	27	(Xue and Cooley, 1993)
								(Senkevich *et al.*, 1993b)
179R	159187	74	8.5	8.5k protein				
B11R	159411	88		VAC	9.2e-43	70/73	95	(Goebel *et al.*, 1990)
				177 matches to glu/asn rich proteins				
180R	159478	283	33.3	protein kinase				(Howard and Smith, 1989)
B12R	160329	283		VAC	1.8e-207	282/283	99	(Goebel *et al.*, 1990)
B12R		134		VAR-1	8.7e-26	31/54	57	(Shchelkunov *et al.*, 1995)
		300		VAC B1R	1.7e-54	26/53	49	(Goebel *et al.*, 1990)
		300		VAR-1 B1R	7.7e-53	25/53	47	(Shchelkunov *et al.*, 1995)
				120 matches mainly to protein kinase family	<0.34			
181R	160437 160787	116	13.0	ICE inhibitor / SPI-2 (f1)				(Kotwal and Moss, 1989) (Smith *et al.*, 1989) (Ray *et al.*, 1992)
B13R				VAC				
B13R		116		VAR-1 (BSH:B12R)	3.0e-72	111/116	95	(Goebel *et al.*, 1990)
		344		CPX crmA	2.7e-69	105/114	92	(Shchelkunov *et al.*, 1995)
		341		VAC C12L (SPI-1)	2.8e-39	66/100	66	(Pickup *et al.*, 1986)
		353		Ectromelia serpin	2.1e-23	25/34	73	(Goebel *et al.*, 1990)
		344		rabbitpox SPI-1	9.2e-23	24/34	70	(Senkevich *et al.*, 1993b)
		357		CPX SPI-1	5.5e-22	25/34	73	(Ali *et al.*, 1994)
		355		VAR-1 B25R (BSH:B21R)	1.4e-21	25/36	69	(Ali *et al.*, 1994)
		372		CPX serpin-like protein	1.7e-21	25/34	73	(Shchelkunov *et al.*, 1995)
		372		135 matches mainly to serpins	1.7e-36	25/36	69	(Ali *et al.*, 1994)
					<0.12			
182R	160762	222	24.9	ICE Inhibitor/SPI-2 (f2)				see above
B14R	161430	222		VAC	6.2e-158	218/222	98	(Goebel *et al.*, 1990)
		345		VAC WR	9.4e-156	215/221	97	(Kotwal and Moss, 1989)
		345		rabbit pox SPI-2	1.6e-153	211/221	95	(Ali *et al.*, 1994)
		341		CPX crmA	4.5e-148	203/220	92	(Pickup *et al.*, 1986)
B13R		344		VAR-1 (BSH:B12R)	1.5e-146	203/220	92	(Shchelkunov *et al.*, 1995)
				309 matches see above	<1.3e-21			
183R	161506	143	16.7	16.7k protein				(Smith and Chan, 1991)
B15R	161937	149		VAC	3.6e-105	97/98	98	(Goebel *et al.*, 1990)
B14R		149		VAR-1(BSH:B13R)	9.1e-104	95/98	96	(Shchelkunov *et al.*, 1995)
		153		VAR-1 D1L (BSH:D2L)	8.8e-31	25/52	48	(Shchelkunov *et al.*, 1995)
		181		VAC C16L/B22R	1.0e-26	25/52	48	(Goebel *et al.*, 1990)
		159		capripox T3A	1.4e-17	17/42	40	(Gershon and Black, 1989a)
		151		rabbit fibroma T3A	2.6e-07	17/44	38	(Upton *et al.*, 1987)
		190		VAC A52R	0.073	10/28	35	(Goebel *et al.*, 1990)
		149		VAC WR K7R	0.21	7/22	31	(Boursnell *et al.*, 1988)
		149		VAR-1 C4R	0.30	7/22	31	(Shchelkunov *et al.*, 1995)
		161		CPX M6R	0.51	7/22	31	(Safronov *et al.*, 1996)
184R	162021 163001	326	36.6	interleukin-1ß receptor (IL-1BR)				(Alcami and Smith, 1992) (Spriggs *et al.*, 1992)
		326		VAC-WR B15R	2.8e-229	323/326	99	(Smith *et al.*, 1991)
		326		CPX B16	2.3e-217	306/326	93	(Spriggs *et al.*, 1992)
B16R		290		VAC	4.4e-202	287/290	98	(Goebel *et al.*, 1990)
B17R		69		VAR-1 (BSH:deleted)	8.1e-38	59/68	86	(Shchelkunov *et al.*, 1995)
		296		HS type II IL-1 receptor	1.7e-36	28/75	37	U64094
				271 matches mainly to IL-1 receptors, growth factor receptors and Ig family proteins	<0.011			
185L	164069	340	39.6	39.6k protein				
B17L	163047	340		VAC	4.8e-248	335/340	98	(Goebel *et al.*, 1990)
B15L		340		VAR-BSH (I:B18L)	2.7e-241	325/340	95	(Shchelkunov *et al.*, 1995)
186R	164209	574	68.0	68k ank-like protein				(Smith *et al.*, 1991)
B18R	165933	574		VAC	0.0	560/574	97	(Goebel *et al.*, 1990)
B19R		574		VAR-1 (BSH:B16R)	0.0	539/574	93	(Shchelkunov *et al.*, 1995)
				100 matches mainly to poxvirus ankyrin proteins	<0.53			
187R	165999 166703	234	27.5	surface antigen, IFN-alpha/beta receptor (f)				(Ueda *et al.*, 1990) (Symons *et al.*, 1995) (Colamonici *et al.*, 1995)
B19R		353		VAC (WR:B18R)	1.4e-163	218/233	93	(Goebel *et al.*, 1990)
B20R		354		VAR-1 (BSH:B17R)	1.53-149	111/133	83	(Shchelkunov *et al.*, 1995)
		569		HS interleukin-1 receptor	0.0051	15/43	34	(McMahan *et al.*, 1991)
				28 matches mainly to IL-1 receptors	<0.53			
188R	167202	70	8.2	8.2k protein (f)				

ORF[a] left	START terminal / STOP	AA[b] region:	kDa[c]	name / (putative) function / homologies[g]	BLAST[d] expect	BLAST[e] AA id	HSS[f] (%)	references
B22R	167414	1897		VAR-BSH (I:B26R)	9.9e-23	31/38	81	(Shchelkunov *et al.*, 1995)
189R	167897	188	21.7	21.7k protein				
B22R	168463	181		VAC B22R/C16L	2.9e-111	95/104	91	(Goebel *et al.*, 1990)
D1L		153		VAR-I(BSH:D2L)	1.2e-88	66/71	92	(Shchelkunov *et al.*, 1995)
		149		VAC B15R	7.2e-19	25/52	48	(Goebel *et al.*, 1990)
		159		capripox T3A	8.0e-05	15/45	33	(Gershon and Black, 1989a)
		151		VAC C6L	0.25	12/46	26	(Goebel *et al.*, 1990)
		156		VAR (I:D9L;BSH:D12L)	0.26	12/46	26	(Shchelkunov *et al.*, 1995)
190R/	168531	233	26.9	45k ank-like protein (f2)				
004L	169232							
B23R		386		VAC (C17L/B23R)	6.2e-159	110/110	100	(Goebel *et al.*, 1990)
D1L		91		VAR-BSH	9.1e-31	46/49	93	(Shchelkunov *et al.*, 1995)
		669		CPX host range	1.1e-13	22/50	44	(Spehner *et al.*, 1988)
		452		VAR-I D6L (BSH:D8L)	1.7e-11	21/50	42	(Shchelkunov *et al.*, 1995)
		574		VAR-I B19R (BSH: B16R)	1.2e-05	22/73	30	(Shchelkunov *et al.*, 1995)
		574		VAC B18R (WR: B17R)	8.6e-05	22/73	30	(Goebel *et al.*, 1990)
		634		VAC C9L	0.00011	11/24	45	(Kotwal and Moss, 1988a)
		585		VAR-I G1R	0.00013	22/74	29	(Shchelkunov *et al.*, 1995)
		516		orf virus	0.0088	15/49	30	(Sullivan *et al.*, 1995b)
		153		VAR-I D7L (BSH:D10L)	0.014	12/28	42	(Shchelkunov *et al.*, 1995)
191R/	169309	102	12.1	45k ank-like protein (f1)				
003L	169617							
B23R		386		VAC C17L/B23R	1.3e-39	62/63	98	(Goebel *et al.*, 1990)
192R/	170305	176	19.7	secr. TNF receptor (f)				(Upton *et al.*, 1991a)
002L	170835	355		CPX crmB	5.1e-71	76/83	91	(Hu *et al.*, 1994)
G2R		348		VAR-BSH	1.0e-66	73/83	87	(Shchelkunov *et al.*, 1995)
		326		Myxoma virus T2	4.9e-30	21/37	56	(Upton *et al.*, 1991a)
		325		Rabbit fibroma Virus T2	1.8e-28	17/36	47	(Upton *et al.*, 1987)
		202		CPX C4L	8.7e-15	30/51	58	(Heller *et al.*, 1990)
B25R		346		HS TNF receptor	1.9e-08	14/26	53	(Safronov *et al.*, 1996)
		259		VAC (*C19L/B25R*)	0.00026	16/19	84	(Goebel *et al.*, 1990)
		277		human CD40L receptor	0.0015	11/24	45	(Stamencovic *et al.*, 1989)
				30 matches to TNF receptors and surface proteins	<0.39			
193R/	171267	136	14.9	35k major secr. protein				(Patel *et al.*, 1990)
001L	171677			chemokine receptor (f)				(Graham *et al.*, 1997)
B29R		244		VAC (*C23L/B29R*)	6.0e-57	41/42	97	(Goebel *et al.*, 1990)
G5R		253		VAR-I	8.9e-51	46/49	93	(Shchelkunov *et al.*, 1995)
		246		CPX ORF B	5.6e-49	40/42	95	(Hu *et al.*, 1994)
		258		SFV T1 protein	2.5e-20	23/42	54	(Upton *et al.*, 1987)
		260		Myxoma virus T1/35kDa	1.5e-14	21/42	50	(Graham *et al.*, 1997)

[a] Open reading frame coding for at least 65 amino acids (for exceptions see text); minor ORFs located in reverse orientation within large ORFs or ORFs located in the repeat regions of the ITRs (see text) are not listed; the MVA ORFs (boldface), listed consecutively as appearing in the genome, and homologs in the Copenhagen strain (in italics), in the variola strains and in the molluscum contagiosum, are listed in this row. Split ORFs are boxed.

[b] Number of deduced amino acids (AA) encoded within an ORF.

[c] Predicted M_r (kDa) for the unmodified protein.

[d] The lowest Poisson probability determined by the BLAST search (Altschul *et al.*, 1990). The Expect value of 0.0 indicates a probability of zero that an alignment occurs by chance; low Expect values correspond to high homology and vice versa.

[e] Amino acid identity (AA id) of first high-scoring segment pair in the BLASTp protocol.

[f] Amino acid identity of first high-scoring segment pair (HSS)%.

[g] Homologies based on searching PIR and SWISS-PROT databases (BLASTp nr).

[h] Duplicated ORFs located in ITRs.

[i] Fragment; complete homologous ORF present in related poxvirus (see reference).

[j] Variola India (I) or variola Bangladesh (BSH) sequences; in cases where the variola sequences are not identical, the variola strain first appearing in the blast search protocol is listed.

[k] ank, ankyrin.

[l] HS, homo sapiens.

[m] MM, *Mus musculus*.

REFERENCES

Adamkiewicz, T. V., McSherry, C., Bach, F. H., and Houchins, J. P. (1994). Natural killer lectin-like receptors have divergent carboxy-termini, distinct from C-type lectins. *Immunogenetics* 39, 218–218.

Ahn, B. Y., Gershon, P. D., Jones, E. V., and Moss, B. (1990a). Identification of rpo30, a vaccinia virus RNA polymerase gene with structural similarity to a eucaryotic transcription elongation factor. *Mol. Cell. Biol.* 10, 5433–5441.

Ahn, B. Y., Jones, E. V., and Moss, B. (1990b). Identification of the vaccinia virus gene encoding an 18-kilodalton subunit of RNA polymerase and demonstration of a 5' poly(A) leader on its early transcript. *J. Virol.* 64, 3019–3024.

Ahn, B. Y., and Moss, B. (1992a). Glutaredoxin homolog encoded by vaccinia virus is a virion-associated enzyme with thioltransferase and dehydroascorbate reductase activities. *Proc. Natl. Acad. Sci. USA* 89, 7060–7064.

Ahn, B. Y., and Moss, B. (1992b). RNA polymerase-associated transcription specificity factor encoded by vaccinia virus. *Proc. Natl. Acad. Sci. USA* 89, 3536–3540.

Ahn, B. Y., Rosel, J., Cole, N. B., and Moss, B. (1992). Identification and expression of rpo19, a vaccinia virus gene encoding a 19-kilodalton DNA-dependent RNA polymerase subunit. *J. Virol.* 66, 971–982.

Akopian, T. A., Kaverina, E. N., Naroditsky, B. S., and Tikhonenko, T. I. (1992). Nucleotide sequence analysis of the avian adenovirus CELO (FAV1) DNA fragment (92-100%). *Mol. Gen. Microbiol. Virol.* 11, 19–23.

Alcami, A., and Smith, G. L. (1992). A soluble receptor for interleukin-1 beta encoded by vaccinia virus: A novel mechanism of virus modulation of the host response to infection. *Cell* 71, 153–167.

Alcami, A., and Smith, G. L. (1995). Vaccinia, cowpox, and camelpox viruses encode soluble gamma interferon receptors with novel broad species specificity. *J. Virol.* 69, 4633–4639.

Ali, A. N., Turner, P. C., Brooks, M. A., and Moyer, R. W. (1994). The SPI-1 gene of rabbitpox virus determines host range and is required for hemorrhagic pock formation. *Virology* 202, 305–314.

Altenburger, W., Suter, C. P., and Altenburger, J. (1989). Partial deletion of the human host range gene in the attenuated vaccinia virus MVA. *Arch. Virol.* 105, 15–27.

Altschul, S. F., and Gish, W. (1996). Local alignment statistics. *Methods Enzymol.* 266, 460–480.

Altschul, S. F., Gish, W., Miller, W., Myers, E. W., and Lipman, D. J. (1990). Basic local alignment search tool. *J. Mol. Biol.* 215, 403–410.

Amegadzie, B. Y., Ahn, B. Y., and Moss, B. (1991a). Identification, sequence, and expression of the gene encoding a Mr 35,000 subunit of the vaccinia virus DNA-dependent RNA polymerase. *J. Biol. Chem.* 266, 13712–13718.

Amegadzie, B. Y., Ahn, B. Y., and Moss, B. (1992). Characterization of a 7-kilodalton subunit of vaccinia virus DNA-dependent RNA polymerase with structural similarities to the smallest subunit of eukaryotic RNA polymerase II. *J. Virol.* 66, 3003–3010.

Amegadzie, B. Y., Holmes, M. H., Cole, N. B., Jones, E. V., Earl, P. L., and Moss, B. (1991b). Identification, sequence, and expression of the gene encoding the second-largest subunit of the vaccinia virus DNA-dependent RNA polymerase. *Virology* 180, 88–98.

Antoine, G., Scheiflinger, F., Holzer, G., Langmann, T., Falkner, F. G., and Dorner, F. (1996). Characterization of the vaccinia MVA hemagglutinin gene locus and its evaluation as an insertion site for foreign genes. *Gene* 177, 43–46.

Baker, M. E., and Blasco, R. (1992). Expansion of the mammalian 3 beta-hydroxysteroid dehydrogenase/plant dihydroflavonol reductase superfamily to include a bacterial cholesterol dehydrogenase, a bacterial UDP-galactose-4-epimerase, and open reading frames in vaccinia virus and fish lymphocystis disease virus. *FEBS Lett.* 301, 89–93.

Banham, A. H., and Smith, G. L. (1992). Vaccinia virus gene B1R encodes a 34-kDa serine/threonine protein kinase that localizes in cytoplasmic factories and is packaged into virions. *Virology* 191, 803–812.

Baylis, C. D., and Smith, G. L. (1997). Vaccinia virion protein VP8, the 25kDa product of the L4R gene, binds single-stranded DNA and RNA with similar affinity. *Nucleic Acids Res.* 25, 3984–3990.

Baylis, S. A., Twigg, S. R., Vydelingum, S., Dixon, L. K., and Smith, G. L. (1993). Three African swine fever virus genes encoding proteins with homology to putative helicases of vaccinia virus. *J. Gen. Virol.* 74, 1969–1974.

Baylis, C. D., and Condit, R. C. (1995). The vaccinia virus A18R gene product is a DNA-dependent ATPase. *J. Biol. Chem.* 270, 1550–1556.

Beattie, E., Tartagia, J., and Paoletti, E. (1991). Vaccinia virus-encoded eIF-2 alpha homolog abrogates the antiviral effect of interferon. *Virology* 183, 419–422.

Bertholet, C., Drillien, R., and Wittek, R. (1985). One hundred base pairs of 5' flanking sequence of a vaccinia virus late gene are sufficient to temporally regulate late transcription. *Proc. Natl. Acad. Sci. USA* 82, 2096–2100.

Binns, M. M., Boursnell, M. E., Tomley, F. M., and Campbell, J. (1989). Analysis of the fowlpoxvirus gene encoding the 4b core polypeptide and demonstration that it possesses efficient promoter sequences. *Virology* 170, 288–291.

Binns, M. M., Britton, B. S., Mason, C., and Boursnell, M. E. (1990). Analysis of the fowlpox virus genome region corresponding to the vaccinia virus D6 to A1 region: Location of, and variation in, non-essential genes in poxviruses. *J. Gen. Virol.* 71, 2873–2881.

Binns, M. M., Stenzler, L., Tomley, F. M., Campbell, J., and Boursnell, M. E. (1987). Identification by a random sequencing strategy of the fowlpoxvirus DNA polymerase gene, its nucleotide sequence and comparison with other viral DNA polymerases. *Nucleic Acids Res.* 15, 6563–6573.

Binns, M. M., Tomley, F. M., Campbell, J., and Boursnell, M. E. (1988). Comparison of a conserved region in fowlpox virus and vaccinia virus genomes and the translocation of the fowlpox virus thymidine kinase gene. *J. Gen. Virol.* 69, 1275–1283.

Blasco, R., Cole, N. B., and Moss, B. (1991). Sequence analysis, expression, and deletion of a vaccinia virus gene encoding a homolog of profilin, a eukaryotic actin-binding protein. *J. Virol.* 65, 4598–4608.

Boursnell, M. E., Foulds, I. J., Campbell, J. I., and Binns, M. M. (1988). Non-essential genes in the vaccinia virus HindIII K fragment: A gene related to serine protease inhibitors and a gene related to the 37K vaccinia virus major envelope antigen. *J. Gen. Virol.* 69, 2995–3003.

Brady, W. A., Kokoris, M. S., Fitzgibbon, M., and Black, M. E. (1996). Cloning, characterization, and modeling of mouse and human guanylate kinases. *J. Biol. Chem.* 271, 16734–16740.

Broyles, S. S., and Fesler, B. S. (1990). Vaccinia virus gene encoding a component of the viral early transcription factor. *J. Virol.* 64, 1523–1529.

Broyles, S. S., and Moss, B. (1986). Homology between RNA polymerases of poxviruses, prokaryotes, and eukaryotes: Nucleotide sequence and transcriptional analysis of vaccinia virus genes encoding 147-kDa and 22-kDa subunits. *Proc. Natl. Acad. Sci. USA* 83, 3141–3145.

Broyles, S. S., and Moss, B. (1987). Identification of the vaccinia virus gene encoding nucleoside triphosphate phosphohydrolase I, a DNA-dependent ATPase. *J. Virol.* 61, 1738–1742.

Broyles, S. S., and Pennington, M. J. (1990). Vaccinia virus gene encoding a 30-kilodalton subunit of the viral DNA-dependent RNA polymerase. *J. Virol.* 64, 5376–5382.

Bult, C. J., White, O., Olsen, G. J., Zhou, L., Fleischmann, R. D., Sutton, G. G., Blake, J. A., and Venter, J. C. (1996). Complete genome sequence of the methanogenic archeon, *Methanococcus jannaschii*. *Science* 273, 1058–1073.

Buyse, I. M., Shao, G., and Huang, S. (1995). The retinoblastoma protein binds to RIZ, a zinc-finger protein that shares an epitope with the adenovirus E1A. *Proc. Natl. Acad. Sci. USA* 92, 4467–4467.

Cabirac, G. F., Strayer, D. S., Sell, S., and Leibowitz, J. L. (1985). Characterization, molecular cloning, and physical mapping of the Shope fibroma virus genome. *Virology* 143, 663–670.

Calvert, J. G., Ogawa, R., Yanagida, N., and Nazerian, K. (1992). Identification and functional analysis of the fowlpox virus homolog of the vaccinia virus p37K major envelope antigen gene. *Virology* 191, 783–792.

Campbell, I. G., Freemont, P. S., Foulkes, W., and Trowsdale, J. (1992). An ovarian tumor marker with homology to vaccinia virus contains an IgV-like region and multiple transmembrane domains. *Cancer Res.* 52, 5416–5420.

Cao, J. X., Gershon, P. D., and Black, D. N. (1995). Sequence analysis of HindIII Q2 fragment of capripoxvirus reveals a putative gene encoding a G-protein-coupled chemokine receptor homologue. *Virology* 209, 207–212.

Cao, J. X., Koop, B. F., and Upton, C. (1997). A human homolog of the vaccinia virus HindIII K4L gene is a member of the phospholipase D superfamily. *Virus Res.* 48, 11–18.

Carroll, M. W., and Moss, B. (1997). Host range and cytopathogenicity of the highly attenuated MVA strain of vaccinia virus: Propagation and generation of recombinant viruses in a nonhuman mammalian cell line. *Virology* 238, 198–205.

Cavallaro, K. F., and Esposito, J. J. (1992). Sequences of the raccoon poxvirus hemagglutinin protein. *Virology* 190, 434–439.

Chang, C., Rodriquez, A., Carretero, M., Lopez-Botet, M., Phillips, J. H., and Lanier, L. L. (1995a). Molecular characterization of human CD94: A type II membrane glycoprotein related to the C-type lectin superfamily. *Eur. J. Immunol.* 25, 2433–2437.

Chang, H. W., Uribe, L. H., and Jacobs, B. L. (1995b). Rescue of vaccinia virus lacking the E3L gene by mutants of E3L. *J. Virol.* 69, 6605–6608.

Chang, H. W., Watson, J. C., and Jacobs, B. L. (1992). The E3L gene of vaccinia virus encodes an inhibitor of the interferon-induced, double-stranded RNA-dependent protein kinase. *Proc. Natl. Acad. Sci. USA* 89, 4825–4829.

Chang-Yeh, A., Mold, D. E., and Huang, R. C. C. (1991). Identification of a novel murine IAP-promoted placenta-expressed gene. *Nucleic Acids Res.* 19, 3667–3672.

Chen, W., Drillien, R., Spehner, D., and Buller, R. M. (1992). Restricted replication of ectromelia virus in cell culture correlates with mutations in virus-encoded host range gene. *Virology* 187, 433–442.

Chertov, O., Telezhinskaya, I. N., Zaitseva, E. V., Golubeva, T. B., Zinov'ev, V. V., Ovechkina, L. G., Mazkova, L. B., and Malygin, E. G. (1991). Amino acid sequence determination of vaccinia virus immunodominant protein p35 and identification of the gene. *Biomed. Sci.* 2, 151–154.

Ciliberto, G., Dente, L., and Cortese, R. (1985). Cell-specific expression of a transfected human alpha1-antitrypsin gene. *Cell*, 531–540.

Colamonici, O. R., Domanski, P., Sweitzer, S. M., Larner, A., and Buller, R. M. (1995). Vaccinia virus B18R gene encodes a type I interferon-binding protein that blocks interferon alpha transmembrane signaling. *J. Biol. Chem.* 270, 15974–15978.

Coppola, T., Waldmann, R., Borsotto, M., Heurteaux, C., Romey, G., Mattei, M. G., and Lazdunski, M. (1994). Molecular cloning of a

murine N-type calcium channel alpha1 subunit. Evidence for isoforms, brain distribution, and chromosomal localization. *FEBS Lett.* 338, 1–5.

Cudmore, S., Blasco, R., Vincentelli, R., Esteban, M., Sodeik, B., Griffiths, G., and Krijnse Locker, J. (1996). A vaccinia virus core protein, p39, is membrane associated. *J. Virol.* 70, 6909–6921.

Davies, M. V., Elroy-Stein, O., Jagus, R., Moss, B., and Kaufman, R. J. (1992). The vaccinia virus K3L gene product potentiates translation by inhibiting double-stranded-RNA-activated protein kinase and phosphorylation of the alpha subunit of eukaryotic initiation factor 2. *J. Virol.* 66, 1943–1950.

Davis, R. E., and Mathews, C. K. (1993). Acidic C terminus of vaccinia virus DNA-binding protein interacts with ribonucleotide reductase. *Proc. Natl. Acad. Sci. USA* 90, 745–749.

Deblandre, G., Marinx, O., Evans, S., Majjaj, S., Leo, O., Caput, D., Huez, G., and Wathelet, M. (1995). Expression cloning of an interferon-inducible 17-kDa membrane protein implicated in the control of cell growth. *J. Biol. Chem.* 270, 23860–23866.

Demkowicz, W. E., Maa, J. S., and Esteban, M. (1992). Identification and characterization of vaccinia virus genes encoding proteins that are highly antigenic in animals and are immunodominant in vaccinated humans. *J. Virol.* 66, 386–398.

Douglas, N. J., and Dumbell, K. R. (1996). DNA sequence variation as a clue to the phylogenesis of orthopoxviruses. *J. Gen. Virol.* 77, 947–951.

Drillien, R., Spehner, D., Villeval, D., and Lecocq, J. P. (1987). Similar genetic organization between a region of fowlpox virus DNA and the vaccinia virus HindIII J fragment despite divergent location of the thymidine kinase gene. *Virology* 160, 203–209.

Dubel, S. J., Starr, T. V. B., Hell, J., Ahlijanian, M. K., Enyeart, J. J., Catterall, W. A., and Snutch, T. P. (1992). Molecular cloning of the alpha-1 subunit of an omega-conotoxin-sensitive calcium channel. *Proc. Natl. Acad. Sci. USA* 89, 5058–5062.

Duncan, S. A., and Smith, G. L. (1992a). Identification and characterization of an extracellular envelope glycoprotein affecting vaccinia virus egress. *J. Virol.* 66, 1610–1621.

Duncan, S. A., and Smith, G. L. (1992b). Vaccinia virus gene SalF5R is non-essential for virus replication in vitro and in vivo. *J. Gen. Virol.* 73, 1235–1242.

Dyster, L. M., and Niles, E. G. (1991). Genetic and biochemical characterization of vaccinia virus genes D2L and D3R which encode virion structural proteins. *Virology* 182, 455–467.

Earl, P. L., Jones; E. V., and Moss, B. (1986). Homology between DNA polymerases of poxviruses, herpesviruses, and adenoviruses: Nucleotide sequence of the vaccinia virus DNA polymerase gene. *Proc. Natl. Acad. Sci. USA* 83, 3659–3663.

Elhabazi, A., Lang, V., Herold, C., Freeman, G. J., Bensussan, A., Boumsell, L., and Bismuth, G. (1997). The human semaphorin-like leukocyte cell surface molecule CD100 associates with a serine kinase activity. *J. Biol. Chem.* 272, 23515–23520.

Engelstad, M., Howard, S. T., and Smith, G. L. (1992). A constitutively expressed vaccinia gene encodes a 42-kDa glycoprotein related to complement control factors that forms part of the extracellular virus envelope. *Virology* 188, 801–810.

Ensser, A., and Fleckenstein, B. (1995). The Alcelaphine herpesvirus type 1 has a semaphorin-like gene. *J. Gen. Virol.* 76, 1063–1067.

Fernando, M. R., Sumimoto, H., Nanri, H., Kawabata, S., Iwanaga, S., Minakami, S., Fukumaki, Y., and Takeshige, K. (1994). Cloning and sequencing of the cDNA encoding human glutaredoxin. *Biochim. Biophys. Acta* 1218, 229–231.

Fleischmann, R. D., Adams, M. D., White, O., Clayton, R. A., Kirkness, E. F., Kerlavage, A. R., Bult, C. J., Tomb, J. F., Dougherty, B. A., and Merrick, J. M. (1995). Whole-genome random sequencing and assembly of Haemophilus influenzae Rd. *Science* 269, 496–512.

Fleming, S. B., Blok, J., Fraser, K. M., Mercer, A. A., and Robinson, A. J. (1993). Conservation of gene structure and arrangement between vaccinia virus and orf virus. *Virology* 195, 175–184.

Franke, C. A., Wilson, E. M., and Hruby, D. E. (1990). Use of a cell-free system to identify the vaccinia virus L1R gene product as the major late myristylated virion protein M25. *J. Virol.* 64, 5988–5996.

Funahashi, S., Sato, T., and Shida, H. (1988). Cloning and characterization of the gene encoding the major protein of the A-type inclusion body of cowpox virus. *J. Gen. Virol.* 69, 35–47.

Furuyama, T., Inagaki, S., Kosugi, A., Noda, S., Saitoh, S., Ogata, M., Iwahashi, Y., Miyazaki, N., Hamaoka, T., and Tohyama, M. (1996). Identification of a novel transmembrane semaphorin expressed on lymphocytes. *J. Biol. Chem.* 271, 33376–33381.

Gershon, P. D., Ahn, B. Y., Garfield, M., and Moss, B. (1991). Poly(A) polymerase and a dissociable polyadenylation stimulatory factor encoded by vaccinia virus. *Cell* 66, 1269–1278.

Gershon, P. D., Ansell, D. M., and Black, D. N. (1989). A comparison of the genome organization of capripoxvirus with that of the orthopoxviruses. *J. Virol.* 63, 4703–4708.

Gershon, P. D., and Black, D. N. (1989a). A capripoxvirus pseudogene whose only intact homologs are in other poxvirus genomes. *Virology* 172, 350–354.

Gershon, P. D., and Black, D. N. (1989b). The nucleotide sequence around the capripoxvirus thymidine kinase gene reveals a gene shared specifically with leporipoxvirus. *J. Gen. Virol.* 70, 525–533.

Gershon, P. D., and Moss, B. (1990). Early transcription factor subunits are encoded by vaccinia virus late genes. *Proc. Natl. Acad. Sci. USA* 87, 4401–4405.

Gershon, P. D., and Moss, B. (1993). Stimulation of poly(A) tail elongation by the VP39 subunit of the vaccinia virus-encoded poly(A) polymerase. *J. Biol. Chem.* 268, 2203–2210.

Gillard, S., Spehner, D., Drillien, R., and Kirn, A. (1986). Localization and sequence of a vaccinia virus gene required for multiplication in human cells. *Proc. Natl. Acad. Sci. USA* 83, 5573–5577.

Giorda, R., Ohmachi, T., and Ennis, H. L. (1989). Organization of a gene family developmentally regulated during *Dictyostelium discoideum* spore germination. *J. Mol. Biol.* 205, 63–69.

Giorda, R., Weisberg, E. P., Ip, T. K., and Trucco, M. (1992). Genomic structure and strain-specific expression of the natural killer cell receptor NKR-P1. *J. Immunol.* 149, 1957–1963.

Goebel, S. J., Johnson, G. P., Perkus, M. E., Davis, S. W., Winslow, J. P., and Paoletti, E. (1990). The complete DNA sequence of vaccinia virus. *Virology* 179, 247–266, 517–563.

Gong, S. C., Lai, C. F., and Esteban, M. (1990). Vaccinia virus induces cell fusion at acid pH and this activity is mediated by the N-terminus of the 14-kDa virus envelope protein. *Virology* 178, 81–91.

Graham, K. A., Lalani, A. S., Macen, J. L., Ness, T. L., Barry, M., Liu, L. Y., Lucas, A., Clark-Lewis, I., Moyer, R. W., and McFadden, G. (1997). The T1/35kDa family of poxvirus-secreted proteins bind chemokines and modulate leukocyte influx into virus-infected tissues. *Virology* 229, 12–24.

Grosenbach, D. W., Ulaeto, D. O., and Hruby, D. E. (1997). Palmitylation of the vaccinia virus 37-kDa major envelope antigen. Identification of a conserved acceptor motif and biological relevance. *J. Biol. Chem.* 272, 1956–1964.

Guan, K. L., Broyles, S. S., and Dixon, J. E. (1991). A Tyr/Ser protein phosphatase encoded by vaccinia virus. *Nature* 350, 359–362.

Gum, J. R. J., Hicks, J. W., Toribara, N. W., Kim, Y. S., and Siddiki, B. (1994). Molecular cloning of human intestinal mucin (MUC2) cDNA: Identification of the amino terminal and overall sequence similarity to pre-pro-von Willebrand factor. *J. Biol. Chem.* 269, 2440–2446.

Gvakharia, B. O., Koonin, E., and Mathews, C. (1996). Vaccinia virus G4L gene encodes a second glutaredoxin. *Virology* 226, 408–411.

Hall, K. T., Boumsell, L., Schultze, J. L., Boussiotis, V. A., Dorfman, D. M., Cardoso, A. A., Bensussan, A., Nadler, L. M., and Freeman, G. J. (1996). Human CD100, a novel leukocyte semaphorin that promotes B-cell aggregation and differentiation. *Proc. Natl. Acad. Sci. USA* 93, 11780–11785.

Hall, R. L., and Moyer, R. W. (1991). Identification, cloning, and sequencing of a fragment of *Amsacta moorei* entomopoxvirus DNA containing the spheroidin gene and three vaccinia virus-related open reading frames. *J. Virol.* 65, 6516–6527.

Hamann, J., Fiebig, H., and Strauss, M. (1993). Molecular cloning of the early activation antigen CD69, a type II integral membrane protein with a C-type lectin domain. *J. Immunol.* 150, 4920–4927.

Hansen, M., Albers, M., Backes, U., Coblenz, A., Leuther, H., Neu, R., Schreer, A., Schafer, B., Zimmerman, M., and Wolf, K. (1996). The sequence of a 23.4 kb segment on the right arm of chromosome VII from *Saccharomyces cerevisiae* reveals CLB6, SPT6, RP28A and NUP57 genes, a Ty3 element and 11 new open reading frames. *Yeast* 12, 1273–1277.

Heller, R. A., Song, K., Onasch, M. A., Fischer, W. H., Chang, D., and Ringold, G. M. (1990). Complementary DNA cloning of a receptor for tumor necrosis factor and demonstration of a shed form of the receptor. *Proc. Natl. Acad. Sci. USA* 87, 6151–6155.

Hirt, P., Hiller, G., and Wittek, R. (1986). Localization and fine structure of a vaccinia virus gene encoding an envelope antigen. *J. Virol.* 58, 757–764.

Hooda-Dhingra, U., Patel, D. D., Pickup, D. J., and Condit, R. C. (1990). Fine structure mapping and phenotypic analysis of five temperature-sensitive mutations in the second largest subunit of vaccinia virus DNA-dependent RNA polymerase. *Virology* 174, 60–69.

Houchins, J. P., Yabe, T., McSherry, C., and Bach, F. H. (1991). DNA sequence analysis of NKG2, a family of related cDNA clones encoding type II integral membrane proteins on human natural killer cells. *J. Exp. Med.* 173, 1017–1020.

Howard, S. T., Chan, Y. S., and Smith, G. L. (1991). Vaccinia virus homologues of the Shope fibroma virus inverted terminal repeat proteins and a discontinuous ORF related to the tumor necrosis factor receptor family. *Virology* 180, 633–647.

Howard, S. T., and Smith, G. L. (1989). Two early vaccinia virus genes encode polypeptides related to protein kinases. *J. Gen. Virol.* 70, 3187–3201.

Hruby, D. E., and Ball, L. A. (1982). Mapping and identification of the vaccinia virus thymidine kinase gene. *J. Virol.* 43, 403–409.

Hu, F. Q., and Pickup, D. J. (1991). Transcription of the terminal loop region of vaccinia virus DNA is initiated from the telomere sequences directing DNA resolution. *Virology* 181, 716–720.

Hu, F. Q., Smith, C. A., and Pickup, D. J. (1994). Cowpox virus contains two copies of an early gene encoding a soluble secreted form of the type II TNF receptor. *Virology* 204, 343–356.

Huang, M. E., Chuat, J. C., and Galibert, F. (1994). A possible yeast homolog of human active-gene-repairing helicase ERCC6. *Biochem. Biophys. Res. Commun.* 201, 310–317.

Hutson, R. A., Zhou, Y., Collins, M. D., Johnson, E. A., Hatheway, C. L., and Sugiyama, H. (1996). Genetic characterization of *Chlostridium botulinum* type A containing silent type B neurotoxin gene sequences. *J. Biol. Chem.* 271, 10786–10792.

Isaacs, S. N., Wolffe, E. J., Payne, L. G., and Moss, B. (1992). Characterization of a vaccinia virus-encoded 42-kilodalton class I membrane glycoprotein component of the extracellular virus envelope. *J. Virol.* 66, 7217–7224.

Jackson, R. J., and Bults, H. G. (1990). A myxoma virus nucleotide sequence with homology to the vaccinia virus RNA polymerase 22-kDa subunit gene. *Nucleic Acids Res.* 18, 5290.

Jackson, R. J., and Bults, H. G. (1992). The myxoma virus thymidine kinase gene: sequence and transcriptional mapping. *J. Gen. Virol.* 73, 323–328.

Jackson, R. J., Hall, D. F., and Kerr, P. J. (1996). Construction of recombinant myxoma viruses expressing foreign genes from different intergenic sites without associated attenuation. *J. Gen. Virol.* 77, 1569–1575.

Jensen, O. N., Houthaeve, T., Shevchenko, A., Cudmore, S., Ashford, T., Mann, M., Griffiths, G., and Krijnse Locker, J. (1996). Identification of the major membrane and core proteins of vaccinia virus by two-dimensional electrophoresis. *J. Virol.* 70, 7485–7497.

Johnson, G. P., Goebel, S. J., Perkus, M. E., Davis, S. W., Winslow, J. P., and Paoletti, E. (1991). Vaccinia virus encodes a protein with similarity to glutaredoxins. *Virology* 181, 378–381.

Kane, E. M., and Shuman, S. (1992). Temperature-sensitive mutations in the vaccinia virus H4 gene encoding a component of the virion RNA polymerase. *J. Virol.* 66, 5752–5762.

Kane, E. M., and Shuman, S. (1993). Vaccinia virus morphogenesis is blocked by a temperature-sensitive mutation in the I7 gene that encodes a virion component. *J. Virol.* 67, 2689–2698.

Kao, S. Y., and Bauer, W. R. (1987). Biosynthesis and phosphorylation of vaccinia virus structural protein VP11. *Virology* 159, 399–407.

Katsanis, N., Fitzgibbon, J., and Fisher, E. M. C. (1996). Paralogy mapping: Identification of a region in the human MHC triplicated onto human chromosomes 1 and 9 allows the prediction and isolation of novel PBX and NOTCH loci. *Genomics* 35, 101–108.

Keck, J. G., Baldick, C. J., Jr., and Moss, B. (1990). Role of DNA replication in vaccinia virus gene expression: A naked template is required for transcription of three late trans-activator genes. *Cell* 61, 801–809.

Keck, J. G., Kovacs, G. R., and Moss, B. (1993). Overexpression, purification, and late transcription factor activity of the 17-kilodalton protein encoded by the vaccinia virus A1L gene. *J. Virol.* 67, 5740–5748.

Kerr, S. M., and Smith, G. L. (1989). Vaccinia virus encodes a polypeptide with DNA ligase activity. *Nucleic Acids Res.* 17, 9039–9050.

Kim, U., Wang, Y., Sanford, T., Zeng, Y., and Nishikura, K. (1994). Molecular cloning of cDNA for double-stranded RNA adenosine deaminase, a candidate enzyme for nuclear RNA editing. *Proc. Natl. Acad. Sci. USA* 91, 11457–11461.

Kolodkin, A. L., Matthes, D. J., and Goodman, C. S. (1993). The semaphorin genes encode a family of transmembrane and secreted growth cone guidance molecules. *Cell* 75, 1389–1399.

Koonin, E. V. (1993). A highly conserved sequence motif defining the family of MutT-related proteins from eubacteria, eukaryotes and viruses. *Nucleic Acids Res.* 21, 4847.

Koonin, E. V., and Senkevich, T. G. (1992). Vaccinia virus encodes four putative DNA and/or RNA helicases distantly related to each other. *J. Gen. Virol.* 73, 989–993.

Koonin, E. V., Senkevich, T. G., and Chernos, V. I. (1993). Gene A32 product of vaccinia virus may be an ATPase involved in viral DNA packaging as indicated by sequence comparisons with other putative viral ATPases. *Virus Genes* 7, 89–94.

Kotwal, G. J. (1996). The great escape. Immune evasion by pathogens. *Immunologist* 4/5, 157–164.

Kotwal, G. J., and Moss, B. (1988a). Analysis of a large cluster of nonessential genes deleted from a vaccinia virus terminal transposition mutant. *Virology* 167, 524–537.

Kotwal, G. J., and Moss, B. (1988b). Vaccinia virus encodes a secretory polypeptide structurally related to complement control proteins. *Nature* 335, 176–178.

Kotwal, G. J., and Moss, B. (1989). Vaccinia virus encodes two proteins that are structurally related to members of the plasma serine protease inhibitor superfamily *J. Virol.* 63, 600–606. [Published erratum appears in *J. Virol.*, 1990, 64(2), 966]

Kovacs, G. R., and Moss, B. (1996). The vaccinia virus H5R gene encodes late gene transcription factor 4: purification, cloning, and overexpression. *J. Virol.* 70, 6796–6802.

Krijnse-Locker, J., Schleich, S., Rodriguez, D., Goud, B., Snijder, E. J., and Griffiths, G. (1996). The role of a 21-kDa viral membrane protein in the assembly of vaccinia virus from the intermediate compartment. *J. Biol. Chem.* 271, 14950–14958.

Kumar, S., and Boyle, D. B. (1990). Mapping of a major early/late gene of fowlpox virus. *Virus Res.* 15, 175–186.

Kwiatkowski, D. J., and Bruns, G. A. P. (1988). Human profilin: Molecular cloning sequence comparison, and chromosomal analysis. *J. Biol. Chem.* 263, 5910–5915.

Ladner, R. D., McNulty, D. E., Carr, S. A., and Roberts, G. D. (1996). Characterization of distinct nuclear and mitochondrial forms of human deoxyuridine triphosphate nucleotidohydrolase. *J. Biol. Chem.* 271, 7745–7751.

Lanier, L. L. (1997). Natural killer cell receptors and MHC class I interactions. *Curr. Opin. Immunol.* 9, 126–131.

Lin, S., and Broyles, S. S. (1994). Vaccinia protein kinase 2: A second essential serine/threonine protein kinase encoded by vaccinia virus. *Proc. Natl. Acad. Sci. USA* 91, 7653–7657.

Lin, S., Chen, W., and Broyles, S. S. (1992). The vaccinia virus B1R gene product is a serine/threonine protein kinase. *J. Virol.* 66, 2717–2723.

Lindberg, F. P., Gresham, H. D., Schwarz, E., and Brown, E. J. (1993). Molecular cloning of integrin-associated protein: An immunoglobulin family member with multiple membrane spanning domains implicated in alpha-v beta-3-dependent ligand binding. *J. Cell. Biol.* 123, 485–496.

Loskutoff, D. J., Linders, M., Keuer, J., Veerman, H., van Heerikhuizen, H., and Pannekoek, H. (1987). Structure of the human plasminogen activator inhibitor 1 gene. Nonrandom distribution of introns. *Biochemistry* 26, 3763–3768.

Maa, J. S., Rodriguez, J. F., and Esteban, M. (1990). Structural and functional characterization of a cell surface binding protein of vaccinia virus. *J. Biol. Chem.* 265, 1569–1577.

Martin, K. H., Grosenbach, D. W., Franke, C. A., and Hruby, D. E. (1997). Identification and analysis of three myristylated vaccinia virus late proteins. *J. Virol.* 71, 5218–5226.

Massung, R. F., Jayarama, V., and Moyer, R. W. (1993). DNA sequence analysis of conserved and unique regions of swinepox virus: Identification of genetic elements supporting phenotypic observations including a novel G protein-coupled receptor homologue. *Virology* 197, 511–528.

Massung, R. F., Liu, L. I., Qi, J., Knight, J. C., Yuran, T. E., Kerlavage, A. R., Parsons, J. M., Venter, J. C., and Esposito, J. J. (1994). Analysis of the complete genome of smallpox variola major virus strain Bangladesh-1975. *Virology* 201, 215–240.

Massung, R. F., Loparev, V. N., Knight, J. C., Totmenin, A. V., Chizhikov, V. E., Parsons, J. M., Safronov, P. F., Gutorov, V. V., Shchelkunov, S. N., and Esposito, J. J. (1996). Terminal region sequence variations in variola virus DNA. *Virology* 221, 291–300.

Massung, R. F., McFadden, G., and Moyer, R. W. (1992). Nucleotide sequence analysis of a unique near-terminal region of the tumorigenic poxvirus, Shope fibroma virus. *J. Gen. Virol.* 73, 2903–2911.

Mayr, A., and Malicki, K. (1966). Attenuierung von virulentem Hühnerpockenvirus in Zellkulturen und Eigenschaften des attenuierten Virus. *Zentralb. Vet. Med. B.* 13, 1–13.

Mayr, A., Stickl, H., Müller, H. K., Danner, K., and Singer, H. (1978). The smallpox vaccination strain MVA: Marker, genetic structure, experience gained with the parenteral vaccination and behavior in organisms with a debilitated defence mechanism. *Zbl. Bakt. Hyg. I.Abt. Orig. B* 167, 375–390.

McIntosh, A. A., and Smith, G. L. (1996). Vaccinia virus glycoprotein A34R is required for infectivity of extracellular enveloped virus. *J. Virol.* 70, 272–281.

McMahan, C. J., Slack, J. L., Mosley, B., Cosman, D., Lupton, S. D., Brunton, L. L., Grubin, C. E., Wignall, J. M., Jenkins, N. A., and Brannan, C. I. (1991). A novel IL-1 receptor, cloned from B cells by mammalian expression, is expressed in many cell types. *EMBO J.* 10, 2821–2832.

Meis, R. J., and Condit, R. C. (1991). Genetic and molecular biological characterization of a vaccinia virus gene which renders the virus dependent on isatin-beta-thiosemicarbazone (IBT). *Virology* 182, 442–454.

Mercer, A. A., Fraser, K. M., Stockwell, P. A., and Robinson, A. J. (1989). A homologue of retroviral pseudoproteases in the parapoxvirus, orf virus. *Virology* 172, 665–668.

Mercer, A. A., Green, G., Sullivan, J. T., Robinson, A. J., and Drillien, R. (1996). Location, DNA sequence and transcriptional analysis of the DNA polymerase gene of orf virus. *J. Gen. Virol.* 77, 1563–1568.

Mercer, A. A., Lyttle, D. J., Whelan, E. M., Fleming, S. B., and Sullivan, J. T. (1995). The establishment of a genetic map of orf virus reveals a pattern of genomic organization that is highly conserved among divergent poxviruses. *Virology* 212, 698–704.

Merchlinsky, M., and Moss, B. (1989). Nucleotide sequence required for resolution of the concatemer junction of vaccinia virus DNA. *J. Virol.* 63, 4354–4361.

Messmer, B., and Dreyer, C. (1993). Requirements for nuclear translocation and nucleolar accumulation of nucleolin of *X. laevis*. *Eur. J. Cell Biol.* 61, 369–382.

Meurs, E., Chong, K., Galabru, J., Thomas, N. S., Kerr, I. M., Williams, B. R., and Hovanessian, A. G. (1990). Molecular cloning and characterization of the human double-stranded RNA-activated protein kinase induced by interferon. *Cell* 62, 379–390.

Meyer, H., Osterrieder, N., and Czerny, C. P. (1994). Identification of binding sites for neutralizing monoclonal antibodies on the 14-kDa fusion protein of orthopox viruses. *Virology* 200, 778–783.

Meyer, H., and Rziha, H. J. (1993). Characterization of the gene encoding the A-type inclusion protein of camelpox virus and sequence comparison with other orthopoxviruses. *J. Gen. Virol.* 74, 1679–1684.

Meyer, H., Sutter, G., and Mayr, A. (1991). Mapping of deletions in the genome of the highly attenuated vaccinia virus MVA and their influence on virulence. *J. Gen. Virol.* 72, 1031–1038.

Miller, C. G., Shchelkunov, S. N., and Kotwal, G. J. (1997). The cowpox virus-encoded homolog of the vaccinia virus complement control protein is an inflammation modulatory protein. *Virology* 229, 126–133.

Moolenaar, W. H., Kranenburg, O., Postma, F. R., and Zondag, G. C. M. (1997). Lysophosphatidic acid: G-protein signalling and cellular responses. *Curr. Opin. Cell Biol.* 9, 168–173.

Moore, J. B., and Smith, G. L. (1992). Steroid hormone synthesis by a vaccinia enzyme: A new type of virus virulence factor *EMBO J.* 11, 1973–1980. [Published erratum appears in *EMBO J.* 1992, 11(9), 3490]

Morgan, J. R., Cohen, L. K., and Roberts, B. E. (1984). Identification of the DNA sequences encoding the large subunit of the mRNA-capping enzyme of vaccinia virus. *J. Virol.* 52, 206–214.

Moss, B. (1996). Poxviridae: The viruses and their replication. *In* "Fields Virology" (B. N. Fields, D. M. Knipe, R. M. Chanock, J. Melnick, B. Roizman, and R. Shope, Eds.). Raven Press, Philadelphia.

Mossman, K., Lee, S. F., Barry, M., Boshkov, L., and McFadden, G. (1996). Disruption of M-T5, a novel myxoma virus gene member of the poxvirus host range superfamily, results in dramatic attenuation of myxomatosis in infected European rabbits. *J. Virol.* 70, 4394–4411.

Mossman, K., Ostergaard, H., Upton, C., and McFadden, G. (1995a). Myxoma virus and Shope fibroma virus encode dual-specificity tyrosine/serine phosphatases which are essential for virus viability. *Virology* 206, 572–582.

Mossman, K., Upton, C., Buller, R. M., and McFadden, G. (1995b). Species specificity of ectromelia virus and vaccinia virus interferon-gamma binding proteins. *Virology* 208, 762–769.

Mustafa, A., and Yuen, L. (1991). Identification and sequencing of the *Choristoneura biennis* entomopoxvirus DNA polymerase gene. *DNA Seq.* 2, 39–45.

Naase, M., Nicholson, B. H., Fraser, K. M., Mercer, A. A., and Robinson, A. J. (1991). An orf virus sequence showing homology to the 14K 'fusion' protein of vaccinia virus: *J. Gen. Virol.* 72, 1177–1181.

Neumann, H., and Zillig, W. (1990). Nucleotide sequence of the viral protein TPX of the TTV1 variant VT3. *Nucleic Acids Res.* 18, 2171.

Niles, E. G., Condit, R. C., Caro, P., Davidson, K., Matusick, L., and Seto, J. (1986). Nucleotide sequence and genetic map of the 16-kb vaccinia virus *Hin*dIII D fragment. *Virology* 153, 96–112.

Niles, E. G., Lee-Chen, G. J., Shuman, S., Moss, B., and Broyles, S. S. (1989). Vaccinia virus gene D12L encodes the small subunit of the viral mRNA capping enzyme. *Virology* 172, 513–522.

Niles, E. G., and Seto, J. (1988). Vaccinia virus gene D8 encodes a virion transmembrane protein. *J. Virol.* 62, 3772–3778.

Nishiyama, Y., Tanaka, T., Naitoh, H., Mori, C., Fukumoto, M., Hiai, H., and Toyokuni, S. (1997). Overexpression of integrin-associated protein (CD47) in rat kidney treated with a renal carcinogen, ferric nitrilotriacetate. *Jpn. J. Cancer Res.* 88, 120–128.

O'Connell, M. A., Krause, S., Higuchi, M., Hsuan, J. J., Totty, N. F., Jenny, A., and Keller, W. (1995). Cloning of cDNAs encoding mammalian double-stranded RNA-specific adenosine deaminase. *Mol. Cell. Biol.* 15, 1389–1397.

Ogawa, R., Calvert, J. G., Yanagida, N., and Nazerian, K. (1993). Insertional inactivation of a fowlpox virus homologue of the vaccinia virus

F12L gene inhibits the release of enveloped virions. *J. Gen. Virol.* 74, 55–64.

Okabe, I., Bailey, L. C., Attree, O., Srinivasan, S., Perkel, J. M., Laurent, B. C., Carlson, M., Nelson, D. L., and Nussbaum, R. L. (1992). Cloning of human and bovine homologs of SNF2/SWI2: A global activator of transcription in yeast *S. cerevisiae*. *Nucleic Acids Res.* 20, 4649–4655.

Osborne, R. J., Symonds, T. M., Sriskantha, A., Lai-Fook, J., Fernon, C. A., and Dall, D. J. (1996). An entomopoxvirus homologue of the vaccinia virus D13L-encoded 'rifampicin resistance' protein. *J. Gen. Virol.* 77, 839–846.

Parkinson, J. E., and Smith, G. L. (1994). Vaccinia virus gene A36R encodes a M(r) 43-50 K protein on the surface of extracellular enveloped virus. *Virology* 204, 376–390.

Parks, R. J., Lichty, B. D., Karakis, C., and Evans, D. H. (1994). Characterization of the Shope fibroma virus DNA ligase gene. *Virology* 202, 642–650.

Passarelli, A. L., Kovacs, G. R., and Moss, B. (1996). Transcription of a vaccinia virus late promoter template: Requirement for the product of the A2L intermediate-stage gene. *J. Virol.* 70, 4444–4450.

Patel, A. H., Gaffney, D. F., Subak-Sharpe, J. H., and Stow, N. D. (1990). DNA sequence of the gene encoding a major secreted protein of vaccinia virus, strain Lister. *J. Gen. Virol.* 71, 2013–2021.

Patel, D. D., and Pickup, D. J. (1989). The second-largest subunit of the poxvirus RNA polymerase is similar to the corresponding subunits of procaryotic and eucaryotic RNA polymerases. *J. Virol.* 63, 1076–1086.

Pena, L., Yanez, R. J., Revilla, Y., Vinuela, E., and Salas, M. L. (1993). African swine fever virus guanylyltransferase. *Virology* 193, 319–328.

Perkus, M. E., Goebel, S. J., Davis, S. W., Johnson, G. P., Limbach, K., Norton, E. K., and Paoletti, E. (1990). Vaccinia virus host range genes. *Virology* 179, 276–286.

Perkus, M. E., Goebel, S. J., Davis, S. W., Johnson, G. P., Norton, E. K., and Paoletti, E. (1991). Deletion of 55 open reading frames from the termini of vaccinia virus. *Virology* 180, 406–410.

Peters, L. L., John, K. M., Lu, F. M., Eicher, E. M., Higgins, A., Yialamas, M., Turtzo, L. C., Otsuka, A. J., and Lux, S. E. (1995). Ank3 (epithelial ankyrin), a widely distributed new member of the ankyrin gene family and the major ankyrin in kidney, is expressed in alternatively spliced forms, including forms that lack the repeat domain. *J. Cell Biol.* 130, 313–330.

Pickup, D. J., Ink, B. S., Hu, W., Ray, C. A., and Joklik, W. K. (1986). Hemorrhage in lesions caused by cowpox virus is induced by a viral protein that is related to plasma protein inhibitors of serine proteases. *Proc. Natl. Acad. Sci. USA* 83, 7698–7702.

Pluciennicczak, A., Schroeder, E., Zettlmeissl, G., and Streeck, R. E. (1985). Nucleotide sequence of a cluster of early and late genes in a conserved segment of the vaccinia virus genome. *Nucleic Acids Res.* 13, 985–998.

Prabhakaran, K., Harris, E. B., and Randhawa, B. (1996). Properties of lysophospholipase in *Mycobacterium leprae*. *J. Basic Microbiol.* 36, 341–349.

Print, C., Leung, E., Harrison, J., and Watoson, J. (1994). Cloning of a gene encoding a human leukocyte protein characterized by extensive heptad repeats. *Gene* 144, 221–228.

Quick, S. D., and Broyles, S. S. (1990). Vaccinia virus gene D7R encodes a 20,000-dalton subunit of the viral DNA-dependent RNA polymerase. *Virology* 178, 603–605.

Ray, C. A., Black, R. A., Kronheim, S. R., Greenstreet, T. A., Sleath, P. R., Salvensen, G. S., and Pickup, D. J. (1992). Viral Inhibition of inflammation: Cowpox virus encodes an inhibitor of the interleukin-1β converting enzyme. *Cell* 69, 597–604.

Reppert, S. M., Weaver, D. R., Cassone, V. M., Godson, C., and Kolakowski, L. F. (1995). Melatonin receptors are for the birds: Molecular analysis of two receptor subtypes differentially expressed in chick brain. *Neuron* 15, 1003–1015.

Rodriguez, D., Esteban, M., and Rodriguez, J. R. (1995). Vaccinia virus A17L gene product is essential for an early step in virion morphogenesis. *J. Virol.* 69, 4640–4648.

Rodriguez, J. F., and Esteban, M. (1987). Mapping and nucleotide sequence of the vaccinia virus gene that encodes a 14-kilodalton fusion protein. *J. Virol.* 61, 3550–3554.

Rodriguez, J. F., Kahn, J. S., and Esteban, M. (1986). Molecular cloning, encoding sequence, and expression of vaccinia virus nucleic acid-dependent nucleoside triphosphatase gene. *Proc. Natl. Acad. Sci. USA* 83, 9566–9570.

Rodriguez, J. F., and Smith, G. L. (1990). IPTG-dependent vaccinia virus: Identification of a virus protein enabling virion envelopment by Golgi membrane and egress. *Nucleic Acids Res.* 18, 5347–5351.

Roper, R. L., Payne, L. G., and Moss, B. (1996). Extracellular vaccinia virus envelope glycoprotein encoded by the A33R gene. *J. Virol.* 70, 3753–3762.

Rosel, J., and Moss, B. (1985). Transcriptional and translational mapping and nucleotide sequence analysis of a vaccinia virus gene encoding the precursor of the major core polypeptide 4b. *J. Virol.* 56, 830–838.

Rosel, J. L., Earl, P. L., Weir, J. P., and Moss, B. (1986). Conserved TAAATG sequence at the transcriptional and translational initiation sites of vaccinia virus late genes deduced by structural and functional analysis of the HindIII H genome fragment. *J. Virol.* 60, 436–449.

Roseman, N. A., Evans, R. K., Mayer, E. L., Rossi, M. A., and Slabaugh, M. B. (1996). Purification and characterization of the vaccinia virus deoxyuridine triphosphatase expressed in *Escherichia coli*. *J. Biol. Chem.* 271, 23506–23511.

Roseman, N. A., and Slabaugh, M. B. (1990). The vaccinia virus *Hin*dIII F fragment: Nucleotide sequence of the left 6.2 kb. *Virology* 178, 410–418.

Ruby, J., Bluethmann, H., Aguet, M., and Ramshaw, I. A. (1995). CD40 ligand has potent antiviral activity. *Nature Med.* 1, 437–441. [See comments]

Safronov, P. F., Petrov, N. A., Riazankina, O. I., Totmenin, A. V., Shchelkunov, S. N., and Sandakhiev, L. S. (1996). Genes of a circle of hosts for the cowpoxvirus. *Dokl. Akad. Nauk.* 349, 829–833.

Sanger, F., Nicklen, S., and Coulson, A. R. (1977). DNA sequencing with chain-terminating inhibitors. *Proc. Natl. Acad. Sci. USA* 74, 5463–5467.

Schmitt, J. F., and Stunnenberg, H. G. (1988). Sequence and transcriptional analysis of the vaccinia virus HindIII I fragment. *J. Virol.* 62, 1889–1897.

Schmutz, C., Payne, L. G., Gubser, J., and Wittek, R. (1991). A mutation in the gene encoding the vaccinia virus 37,000-M(r) protein confers resistance to an inhibitor of virus envelopment and release. *J. Virol.* 65, 3435–3442.

Schneider, S. S., Schick, C., Fish, K. E., Miller, E., Pena, J. C., Treter, S., Hui, S. M., and Silverman, G. A. (1995). A serine proteinase inhibitor locus at 18q21.3 contains a tandem duplication of the human squamous cell carcinoma antigen gene. *Proc. Natl. Acad. Sci. USA* 92, 3147–3151.

Schnitzlein, W. M., and Tripathy, D. N. (1991). Identification and nucleotide sequence of the thymidine kinase gene of swinepox virus. *Virology* 181, 727–732.

Schweizer, M., and Neumann-Haefelin, D. (1995). Phylogenetic analysis of primate foamy virus by comparison of pol sequences. *Virology* 207, 577–582.

Senkevich, T. G., Bugert, J. J., Sisler, J. R., Koonin, E. V., Darai, G., and Moss, B. (1996). Genome sequence of a human tumorigenic poxvirus: prediction of specific host response-evasion genes. *Science* 273, 813–816.

Senkevich, T. G., Koonin, E. V., Bugert, J. J., Darai, G., and Moss, B. (1997). The genome of molluscum contagiosum virus: analysis and comparison with other poxviruses. *Virology* 233, 19–42.

Senkevich, T. G., Koonin, E. V., and Buller, R. M. (1993a). A poxvirus protein with a RING zinc finger motif is of crucial importance for virulence. *Virology* 198, 118–128.

Senkevich, T. G., Muravnik, G. L., Pozdnyakov, S. G., Chizhkov, V. E., Ryazankina, O. I., Shchelkunov, S. N., Koonin E. V., and Chernos, V. I.

(1993b). Nucleotide sequence of XhoI O fragment of ectromelia virus DNA reveals significant differences from vaccinia virus. *Virus Res.* 30, 73–88.

Seralini, G. E., Underhill, C. M., Smith, C. L., Nguyen, V. T., and Hammond, G. L. (1989). Biological half-life and transfer of maternal corticosteroid-binding globulin to amniotic fluid in the rabbit. *Endocrinology* 125, 1321–1325.

Shchelkunov, S. N., Blinov, V. M., Resenchuk, S. M., Totmenin, A. V., and Sandakhchiev, L. S. (1993a). Analysis of the nucleotide sequence of a 43 kbp segment of the genome of variola virus India-1967 strain. *Virus Res.* 30, 239–258.

Shchelkunov, S. N., Blinov, V. M., and Sandakhchiev, L. S. (1993b). Ankyrin-like proteins of variola and vaccinia viruses. *FEBS Lett.* 319, 163–165.

Shchelkunov, S. N., Blinov, V. M., Totmenin, A. V., Marennikova, S. S., Kolykhalov, A. A., Frolov, I. V., Chizhikov, V. E., Gytorov, V. V., Gashikov, P. V., and Belanov, E. F. (1993c). Nucleotide sequence analysis of variola virus HindIII M, L, I genome fragments. *Virus Res.* 27, 25–35.

Shchelkunov, S. N., Marennikova, S. S., Blinov, V. M., Resenchuk, S. M., Totmenin, A. V., Chizhikov, V. E., Guturov, V. V., Safronov, P. F., Kurmanov, R. K., and Sandakhchiev, L. S. (1993d). Entire coding sequence of the variola virus. *Dokl. Akad. Nauk.* 328, 629–632.

Shchelkunov, S. N., Massung, R. F., and Esposito, J. J. (1995). Comparison of the genome DNA sequences of Bangladesh-1975 and India-1967 variola viruses. *Virus Res.* 36, 107–118.

Shida, H. (1986). Nucleotide sequence of the vaccinia virus hemagglutinin gene. *Virology* 150, 451–462.

Shuman, S. (1992). Vaccinia virus RNA helicase: An essential enzyme related to the DE-H family of RNA-dependent NTPases. *Proc. Natl. Acad. Sci. USA* 89, 10935–10939.

Shuman, S., and Moss, B. (1987). Identification of a vaccinia virus gene encoding a type I DNA topoisomerase. *Proc. Natl. Acad. Sci. USA* 84, 7478–7482.

Skimmer, M. A., Moore, J. B., Binns, M. M., Smith, G. L., and Boursnell, M. E. (1994). Deletion of fowlpox virus homologues of vaccinia virus genes between the 3 beta-hydroxysteroid dehydrogenase (A44L) and DNA ligase (A50R) genes. *J. Gen. Virol.* 75, 2495–2498.

Slabaugh, M., Roseman, N., Davis, R., and Mathews, C. (1988). Vaccinia virus-encoded ribonucleotide reductase: Sequence conservation of the gene for the small subunit and its amplification in hydroxyurea-resistant mutants. *J. Virol.* 62, 519–527.

Smith, G. L., and Chan, Y. S. (1991). Two vaccinia virus proteins structurally related to the interleukin-1 receptor and the immunoglobulin superfamily. *J. Gen. Virol.* 72, 511–518.

Smith, G. L., Chan, Y. S., and Howard, S. T. (1991). Nucleotide sequence of 42 kbp of vaccinia virus strain WR from near the right inverted terminal repeat. *J. Gen. Virol.* 72, 1349–1376.

Smith, G. L., Howard, S. T., and Chan, Y. S. (1989). Vaccinia virus encodes a family of genes with homology to serine proteinase inhibitors. *J. Gen. Virol.* 70, 2333–2343.

Spehner, D., Gillard, S., Drillien, R., and Kirn, A. (1988). A cowpox virus gene required for multiplication in Chinese hamster ovary cells. *J. Virol.* 62, 1297–1304.

Spriggs, M. K., Hruby, D. E., Maliszewski, C. R., Pickup, D. J., Sims, J. E., Buller, R. M., and VanSlyke, J. (1992). Vaccinia and cowpox viruses encode a novel secreted interleukin-1-binding protein. *Cell* 71, 145–152.

Stamencovic, I., Clark, E. A., and Seed, B. (1989). A B-lymphocyte activation molecule related to the nerve growth factor receptor and induced by cytokines in carcinomas. *EMBO J.* 8, 1403–1410.

Strayer, D. S., Jerng, H. H., and O'Connor, K. (1991). Sequence and analysis of a portion of the genomes of Shope fibroma virus and malignant rabbit fibroma virus that is important for viral replication in lymphocytes. *Virology* 185, 585–595.

Stroobant, P., Rice, A. P., Gullick, W. J., Cheng, D. J., Kerr, I. M., and Waterfield, M. D. (1985). Purification and characterization of vaccinia virus growth factor. *Cell* 42, 383–393.

Sullivan, J. T., Fleming, S. B., Robinson, A. J., Mercer, A. A. (1995a). Sequence and transcriptional analysis of a near-terminal region of the orf virus genome. *Virus Genes* 11, 21–29.

Sullivan, J. T., Fraser, K. M., Fleming, S. B., Robinson, A. J., and Mercer, A. A. (1995b). Sequence and transcriptional analysis of an orf virus gene encoding ankyrin- like repeat sequences. *Virus Genes* 9, 277–282.

Sullivan, J. T., Mercer, A. A., Fleming, S. B., and Robinson, A. J. (1994). Identification and characterization of an orf virus homologue of the vaccinia virus gene encoding the major envelope antigen p37K. *Virology* 202, 968–973.

Sung, T. C., Roper, R. L., Zhang, Y., Rudge, S. A., Temel, R., Hammond, S. M., Morris, A. J., Moss, B., Engebrecht, J., and Frohman, M. A. (1997). Mutagenesis of phospholipase D defines a superfamily including a trans-Golgi viral protein required for poxvirus pathogenicity. *EMBO J.* 16, 4519–4530.

Sutter, G., and Moss, B. (1992). Nonreplicating vaccinia vector efficiently expresses recombinant genes. *Proc. Natl. Acad. Sci. USA* 89, 10847–10851.

Sutter, G., Wyatt, L. S., Foley, P. L., Bennink, J. R., and Moss, B. (1994). A recombinant vector derived from the host range-restricted and highly attenuated MVA strain of vaccinia virus stimulates protective immunity in mice to influenza virus. *Vaccine* 12, 1032–1040.

Symons, J. A., Alcami, A., and Smith, G. L. (1995). Vaccinia virus encodes a soluble type I interferon receptor of novel structure and broad species specificity. *Cell* 81, 551–560.

Takahashi, R., Oie, M., and Ichihashi, Y. (1994). N-terminal amino acid sequences of vaccinia virus structural proteins. *Virology* 202, 844–852.

Takahashi-Nishimaki, F., Funahashi, S., Miki, K., Hashizume, S., and Sugimoto, M. (1991). Regulation of plaque size and host range by a vaccinia virus gene related to complement system proteins. *Virology* 181, 158–164.

Talbott, R. L., Sparger, E. E., Lovelace, K. M., Fitch, W. M., Pedersen, N. C., Luciw, P. A., and Elder, J. H. (1989). Nucleotide sequence and genomic organization of feline immunodeficiency virus. *Proc. Natl. Acad. Sci. USA* 86, 5743–5747.

Tamin, A., Esposito, J., and Hruby, D. (1991). A single nucleotide substitution in the 5'-untranslated region of the vaccinia N2L gene is responsible for both alpha-amanitin-resistant and temperature-sensitive phenotypes. *Virology* 182, 393–396.

Tan, J. L., and Spudich, J. A. (1990). Developmentally regulated protein-tyrosine kinase genes in *Dictyostelium discoideum*. *Mol. Cell. Biol.* 10, 3578–3583.

Tartaglia, J., Perkus, M. E., Taylor, J., Norton, E. K., Audonnet, J. C., Cox, W. I., Davis, S. W., van der Hoeven, J., Meignier, B., Riviere, M., Languet, B., and Paoletti, E. (1992). NYVAC: A highly attenuated strain of vaccinia virus. *Virology* 188, 217–232.

Tartaglia, J., and Paoletti, E. (1985). Physical mapping and DNA sequence analysis of the rifampicin resistance locus in vaccinia virus. *Virology* 147, 394–404.

Tartaglia, J., Winslow, J., Goebel, S., Johnson, G. P., Taylor, J., and Paoletti, E. (1990). Nucleotide sequence analysis of a 10.5 kbp HindIII fragment of fowlpox virus: Relatedness to the central portion of the vaccinia virus HindIII D region. *J. Gen. Virol.* 71, 1517–1524.

Tengelsen, L. A., Slabaugh, M. B., Bibler, J. K., and Hruby, D. E. (1988). Nucleotide sequence and molecular genetic analysis of the large subunit of ribonucleotide reductase encoded by vaccinia virus. *Virology* 164, 121–131.

Tomley, F., Binns, M., Campbell, J., and Boursnell, M. (1988). Sequence analysis of an 11.2 kilobase, near-terminal, BamHI fragment of fowlpox virus. *J. Gen. Virol.* 69, 1025–1040.

Twardzik, D. R., Brown, J. P., Ranchalis, J. E., Todaro, G. J., and Moss, B. (1985). Vaccinia virus-infected cells release a novel polypeptide functionally related to transforming and epidermal growth factors. *Proc. Natl. Acad. Sci. USA* 82, 5300–5304.

Ueda, Y., Morikawa, S., and Matsuura, Y. (1990). Identification and nucleotide sequence of the gene encoding a surface antigen induced by vaccinia virus. *Virology* 177, 588–594.

Upton, C., DeLange, A. M., and McFadden, G. (1987). Tumorigenic poxviruses: genomic organization and DNA sequence of the telomeric region of the Shope fibroma virus genome. *Virology* 160, 20–30.

Upton, C., Macen, J. L., Schreiber, M., and McFadden, G. (1991a). Myxoma virus expresses a secreted protein with homology to the tumor necrosis factor receptor family that contributes to viral virulence. *Virology* 184, 370–382.

Upton, C., Macen, J. L., Wishart, D. S., and McFadden, G. (1990a). Myxoma virus and malignant rabbit fibroma virus encode a serpin-like protein important for virus virulence. *Virology* 179, 618–631.

Upton, C., Mossman, K., and McFadden, G. (1992). Encoding of a homolog of the IFN-g receptor by myxoma virus. *Science* 258, 1369–1372.

Upton, C., Opgenorth, A., Traktman, P., and McFadden, G. (1990b). Identification and DNA sequence of the Shope fibroma virus DNA topoisomerase gene. *Virology* 176, 439–447.

Upton, C., Stuart, D., and McFadden, G. (1991b). Identification and DNA sequence of the large subunit of the capping enzyme from Shope fibroma virus. *Virology* 183, 773–777.

Upton, C., Stuart, D. T., and McFadden, G. (1993). Identification of a poxvirus gene encoding a uracil DNA glycosylase. *Proc. Natl. Acad. Sci. USA* 90, 4518–4522.

Van Meir, E., and Wittek, R. (1988). Fine structure of the vaccinia virus gene encoding the precursor of the major core protein 4a. *Arch. Virol.* 102, 19–27.

Vanslyke, J. K., Whitehead, S. S., Wilson, E. M., and Hruby, D. E. (1991). The multistep proteolytic maturation pathway utilized by vaccinia virus P4a protein: A degenerate conserved cleavage motif within core proteins. *Virology* 183, 467–478.

Vassalli, J. D., Huarte, J., Bosco, D., Sappino, A. P., Sappino, N., Velardi, A., Wohlwend, A., Erno, H., Monard, D., and Belin, D. (1993). Protease-nexin 1 as an androgen-dependent secretory product of the murine seminal vesicle. *EMBO J.* 12, 1871–1898.

Venkatesan, S., Gershowitz, A., and Moss, B. (1982). Complete nucleotide sequences of two adjacent early vaccinia virus genes located within the inverted terminal repetition. *J. Virol.* 44, 637–646.

Vos, J. C., Sasker, M., and Stunnenberg, H. G. (1991). Vaccinia virus capping enzyme is a transcription initiation factor. *EMBO J.* 10, 2553–2558.

Vydelingum, S., Baylis, S. A., Bristow, C., Smith, G. L., and Dixon, L. K. (1993). Duplicated genes within the variable right end of the genome of a pathogenic isolate of African swine fever virus. *J. Gen. Virol.* 74, 2125–2130.

Wang, S., and Shuman, S. (1995). Vaccinia virus morphogenesis is blocked by temperature-sensitive mutations in the F10 gene, which encodes protein kinase 2. *J. Virol.* 69, 6376–6388.

Way, M., Sanders, M., Chafel, M., Tu, Y. H., Knight, A., and Matsudaira, P. (1995). Beta-scruin, a homolog of the actin crosslinking protein scruin, is localized to the acrosomal vesicle of Limulus sperm. *J. Cell. Sci.* 108, 3155–3162.

Wei, Y. F., Robins, P., Carter, K., Caldecott, K., Pappin, D. J. C., Yu, G. L., Wang, R. P., Shell, B. K., Nash, R., Schar, P., Barnes, D. E., Haseltine, W. A., and Lindahl, T. Molecular cloning and expression of human cDNAs encoding a novel DNA ligase IV and DNA ligase III, an enzyme active in DNA repair and recombination. *Mol. Cell. Biol.* 15, 3206–3216.

Weinrich, S. L., and Hruby, D. E. (1986). A tandemly-oriented late gene cluster within the vaccinia virus genome. *Nucleic Acids Res.* 14, 3003–3016.

Weir, J. P., and Moss, B. (1983). Nucleotide sequence of the vaccinia virus thymidine kinase gene and the nature of spontaneous frameshift mutation. *J. Virol.* 46, 530–537.

Whayeb, S. H., Yamamoto, K., Tojo, H., and Honda, T. (1996). Genetic analysis of the chromosomal region encoding lysophospholipase L2 of Vibrio cholerae O1. *Biochim. Biophys. Acta* 1300, 1–4.

Wilson, R., Ainscough, R., Anderson, K., Baynes, C., Berks, M., Bonfield, J., Burton, J., Connell, M., Copsey, T., Cooper, J., Coulson, A., Craxton, M., Dear, S., Du, Z., Durbin, R., Favello, A., Fulton, L., Gardner, A., Green, P., Hawkins, T., Hillier, L., Jier, M., Johnston, L., Jones, M., Kershaw, J., Kirsten, J., Laister, N., Latreille, P., Lightning, J., Lloyd, C., McMurray, A., Mortimore, B., O'Callaghan, M., Parsons, J., Percy, C., Rifken, L., Roopra, A., Saunders, D., Shownkeen, R., Smaldon, N., Smith, A., Sonnhammer, E., Staden, R., Sulston, J., Thierry-Mieg, J., Thomas, K., Vaudin, M., Vaughan, K., Waterston, R., Watson, A., Weinstock, L., Wilkinson-Sproat, J., and Wohldman, P. (1994). 2.2 Mb of contiguous nucleotide sequence from chromosome III of *C. elegans*. *Nature* 368, 32–38.

Wolffe, E. J., Katz, E., Weisberg, A., and Moss, B. (1997). The A34R glycoprotein gene is required for induction of specialized actin-containing microvilli and efficient cell-to-cell transmission of vaccinia virus. *J. Virol.* 71, 3904–3915.

Wolffe, E. J., Moore, D. M., Peters, P. J., and Moss, B. (1996). Vaccinia virus A17L open reading frame encodes an essential component of nascent viral membranes that is required to initiate morphogenesis. *J. Virol.* 70, 2797–2808.

Wright, C. F., Keck, J. G., Tsai, M. M., and Moss, B. (1991). A transcription factor for expression of vaccinia virus late genes is encoded by an intermediate gene. *J. Virol.* 65, 3715–3720.

Xue, F., and Cooley, L. (1993). Kelch encodes a component of intercellular bridges in Drosophila egg chambers. *Cell* 72, 681–693.

Yanez, R. J., Rodriquez, J. M., Nogal, M. L., Yuste, L., Enriques, C., Rodriguez, J. F., and Vinuela, E. (1993). Analysis of the complete nucleotide sequence of African Swine Fever Virus. *Virology* 208, 249–278.

Yang, W. P., and Bauer, W. R. (1988). Purification and characterization of vaccinia virus structural protein VP8. *Virology* 167, 578–584.

Yuen, L., Noiseux, M., and Gomes, M. (1991). DNA sequence of the nucleoside triphosphate phosphohydrolase I (NPH I) of the *Choristoneura biennis* entomopoxvirus. *Virology* 182, 403–406.

Zantinge, J. L., Krell, P. J., Derbyshire, J. B., and Nagy, E. (1996). Partial transcriptional mapping of the fowlpox virus genome and analysis of the EcoRI L fragment. *J. Gen. Virol.* 77, 603–614.

Zhang, H., Scheirer, D. C., Fowle, W. H., and Goodman, H. M. (1992). Expression of antisense gene blocks chloroplast differentiation in Arabidopsis. *Plant Cell* 4, 1575–1588.